GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 18:13:48 ; Search time 13687 Seconds
(without alignments)
11466.729 Million cell updates/sec

Title: US-10-045-072-1
Perfect score: 3621
Sequence: 1 tggggcggggttagatcctg.....tgatcgtcgtcgtttcctaa 3621

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		3621	100.0	3621	6	AR123974	AR123974 Sequence
2		3621	100.0	3621	6	AR213173	AR213173 Sequence
3		3621	100.0	3637	1	AF038548	AF038548 Corynebac
4		3621	100.0	332050	1	AP005276	AP005276 Corynebac
5		3621	100.0	349980	6	AX127145	AX127145 Sequence
6		3578	98.8	3728	1	CGPYC	Y09548 Corynebacte
7		3578	98.8	3728	6	A97276	A97276 Sequence 1
8		3578	98.8	3728	6	BD140686	BD140686 Method fo
9		3469	95.8	3657	1	AF503915	AF503915 Corynebac
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12		3398.8	93.9	3474	6	AX453601	AX453601 Sequence
13		3398.8	93.9	3474	6	AX453603	AX453603 Sequence
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17		1927.4	53.2	341553	1	BX248355	BX248355 Corynebac
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19		1395	38.5	1406	6	AX064995	AX064995 Sequence
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21		1328.2	36.7	4218	1	AF262949	AF262949 Mycobacte
c 22		1294.4	35.7	17992	1	AE007125	AE007125 Mycobacte
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36		714	19.7	3994	4	AY185595	AY185595 Bos tauru
37		707.8	19.5	3537	4	AY225510	AY225510 Sus scrof
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40		701.2	19.4	3559	5	AF509529	AF509529 Gallus ga
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ALIGNMENTS

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LOCUS AR123974 3621 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6171833.
ACCESSION AR123974
VERSION AR123974.1 GI:14109335
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3621)
AUTHORS Sinskey,A.J., Lessard,P.A. and Willis,L.B.
TITLE Pyruvate carboxylase from corynebacterium glutamicum
JOURNAL Patent: US 6171833-A 1 09-JAN-2001;
FEATURES Location/Qualifiers

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/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 3621; DB 6; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from patent US 6403351.
ACCESSION AR213173
VERSION AR213173.1 GI:23310240
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3621)
AUTHORS Sinskey,A.J., Lessard,P.A. and Willis,L.B.
TITLE Pyruvate carboxylase polypeptide from Corynebacterium glutamicum
JOURNAL Patent: US 6403351-A 1 11-JUN-2002;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 3621; DB 6; Length 3621;
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Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
Qy       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
Db       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320

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Qy       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
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Qy       3601 TTGATCGTCGTCGTTTCCTAA 3621
Db       3601 TTGATCGTCGTCGTTTCCTAA 3621
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RESULT 3
AF038548

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LOCUS       AF038548               3637 bp    DNA     linear   BCT 25-AUG-2000
DEFINITION  Corynebacterium glutamicum pyruvate carboxylase (pyc) gene,
            complete cds.
ACCESSION   AF038548
VERSION     AF038548.1  GI:2708716
KEYWORDS    .
SOURCE      Corynebacterium glutamicum
  ORGANISM  Corynebacterium glutamicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1  (bases 1 to 3637)
  AUTHORS   Koffas,M.A., Ramamoorthi,R., Pine,W.A., Sinskey,A.J. and
            Stephanopoulos,G.
  TITLE     Sequence of the Corynebacterium glutamicum pyruvate carboxylase
            gene
  JOURNAL   Appl. Microbiol. Biotechnol. 50 (3), 346-352 (1998)
  MEDLINE   99019028
   PUBMED   9802220
REFERENCE   2  (bases 1 to 3637)
  AUTHORS   Koffas,M.A.G., Ramamoorthi,R., Pine,W.A., Sinskey,A.J. and
            Stephanopoulos,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-DEC-1997) Chemical Engineering, Massachusetts
            Insitute of Technology, 77 Massachusetts Avenue, Cambridge, MA
            02139, USA
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ORIGIN

Query Match 100.0%; Score 3621; DB 1; Length 3637;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180
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Db        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180

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ACCESSION   AP005276 BA000036
VERSION     AP005276.1  GI:21323419
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SOURCE      Corynebacterium glutamicum ATCC 13032
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REFERENCE   1
  AUTHORS   Nakagawa,S.
  TITLE     Complete genomic sequence of Corynebacterium glutamicum ATCC 13032
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 332050)
  AUTHORS   Nakagawa,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.
            Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,
            Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com,
            Tel:81-44-829-3031, Fax:81-44-813-1651)
COMMENT     This sequence is conducted by collaboration of Kyowa Hakko Kogyo
            Co. Ltd. And Kitasato University.
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RESULT 5
AX127145
LOCUS       AX127145               349980 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 7061 from Patent EP1108790.
ACCESSION   AX127145 AX114121
VERSION     AX127145.1  GI:14041133
KEYWORDS    .
SOURCE      Corynebacterium glutamicum
  ORGANISM  Corynebacterium glutamicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1
  AUTHORS   Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
  TITLE     Novel polynucleotides
  JOURNAL   Patent: EP 1108790-A 7061 20-JUN-2001;
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FEATURES             Location/Qualifiers
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                     0.600.001 0.949.980 '"
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3621;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     105013 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 105072

Qy         61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120
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Qy        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180
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Qy        241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300
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Qy        301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360
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Qy        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660
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Qy        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
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Qy        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
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Qy        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
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Qy       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
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Db     108133 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 108192
Qy       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
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RESULT 6
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DEFINITION  Corynebacterium glutamicum pyc gene.
ACCESSION   Y09548
VERSION     Y09548.1  GI:2879822
KEYWORDS    pyc gene; pyruvate carboxylase.
SOURCE      Corynebacterium glutamicum
  ORGANISM  Corynebacterium glutamicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1
  AUTHORS   Peters-Wendisch,P.G., Kreutzer,C., Kalinowski,J., Patek,M., Sahm,H.
            and Eikmanns,B.J.
  TITLE     Pyruvate carboxylase from Corynebacterium glutamicum:
            characterization, expression and inactivation of the pyc gene
  JOURNAL   Microbiology (Reading, Engl.) 144 (Pt 4), 915-927 (1998)
  MEDLINE   98240228
   PUBMED   9579065
REFERENCE   2  (bases 1 to 3728)
  AUTHORS   Peters-Wendisch,P.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-1996) P.G. Peters-Wendisch, Institut fuer
            Biotechnologie 1, Forschungszentrum Juelich GmbH, Juelich, D-52425,
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ORIGIN

Query Match 98.8%; Score 3578; DB 1; Length 3728;
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Matches 3578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     704 CAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCA 763
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Qy     884 GAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTG 943
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Qy     944 TCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATG 1003
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Qy    1004 CAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCG 1063
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ACCESSION   A97276
VERSION     A97276.1  GI:6780661
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SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3728)
  AUTHORS   Peters-Wendisch,P. and Eikmanns,B.
  TITLE     METHOD FOR MICROBIAL PRODUCTION OF AMINO ACIDS OF THE ASPARTATE
            AND/OR GLUTAMATE FAMILY AND AGENTS WHICH CAN BE USED IN SAID METHOD
  JOURNAL   Patent: WO 9918228-A 1 15-APR-1999;
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ORIGIN
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Qy        344 CATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCA 403
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        464 TTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAA 523
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 ACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTC 549

Qy        584 GCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCA 643
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        644 AAAACATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGG 703
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAAACATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGG 669

Qy        704 CAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCA 763
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        764 AATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATG 823
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Db        730 AATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATG 789

Qy        824 TCGAACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTG 883
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Qy        944 TCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATG 1003
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Db        1570 AGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGC 1629

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Db       2710 CACTGGGCCTTGCGGATCGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGA 2769
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RESULT 8
BD140686

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LOCUS       BD140686                3728 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method for microbial production of amino acids of the aspartate
            and/or glutamate family and agents which can be used in said
            method.
ACCESSION   BD140686
VERSION     BD140686.1  GI:23235631
KEYWORDS    JP 2002508921-A/1.
SOURCE      Corynebacterium glutamicum
  ORGANISM  Corynebacterium glutamicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1  (bases 1 to 3728)
  AUTHORS   Eikmanns,B., Wendisch,P.P. and Sahm,H.
  TITLE     Method for microbial production of amino acids of the aspartate
            and/or glutamate family and agents which can be used in said method
  JOURNAL   Patent: JP 2002508921-A 1 26-MAR-2002;
            FORSCHUNGSZENTRUM JULICH GMBH
COMMENT     OS   Corynebacterium glutamicum
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            PD   26-MAR-2002
            PF   30-SEP-1998 JP 2000515022
            PR   04-OCT-1997 DE 197 43 894.6,14-JUL-1998 DE 198 31 609.7 PI
            BERND EIKMANNS,PETRA PETERS WENDISCH,HERMANN SAHM PC
            C12N15/09,C12N1/21,C12P13/20//(C12P13/20,C12R1:15),C12N15/00 CC
            pyruvate carboxylase gene
            FH   Key             Location/Qualifiers
            FT   CDS             (165). .(3587).
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 98.8%; Score 3578; DB 6; Length 3728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         44 GCTTGAAGTCGTGCAGGTCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAAC 103
Db         10 GCTTGAAGTCGTGCAGGTCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAAC 69
Qy        104 CGATGTTTGATTGGGGGAATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCC 163
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Qy       344 CATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCA 403
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Db       370 AGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCA 429
Qy       464 TTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAA 523
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RESULT 9
AF503915

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DEFINITION  Corynebacterium crenatum strain CD945 pyruvate carboxylase (pyc)
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ACCESSION   AF503915
VERSION     AF503915.1  GI:20531756
KEYWORDS    .
SOURCE      Corynebacterium crenatum
  ORGANISM  Corynebacterium crenatum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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REFERENCE   1  (bases 1 to 3657)
  AUTHORS   Wang,J., Ding,J. and Liu,Y.
  TITLE     Cloning and Expression of Pyruvate Carboxylase Gene in
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3657)
  AUTHORS   Wang,J., Ding,J. and Liu,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-2002) Center of Microbial Biotechnology,
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ORIGIN

Query Match 95.8%; Score 3469; DB 1; Length 3657;
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RESULT 10
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DEFINITION Sequence 765 from Patent EP1108790.
ACCESSION AX120849
VERSION AX120849.1 GI:14037564
KEYWORDS .
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE Novel polynucleotides
JOURNAL Patent: EP 1108790-A 765 20-JUN-2001;
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ORIGIN

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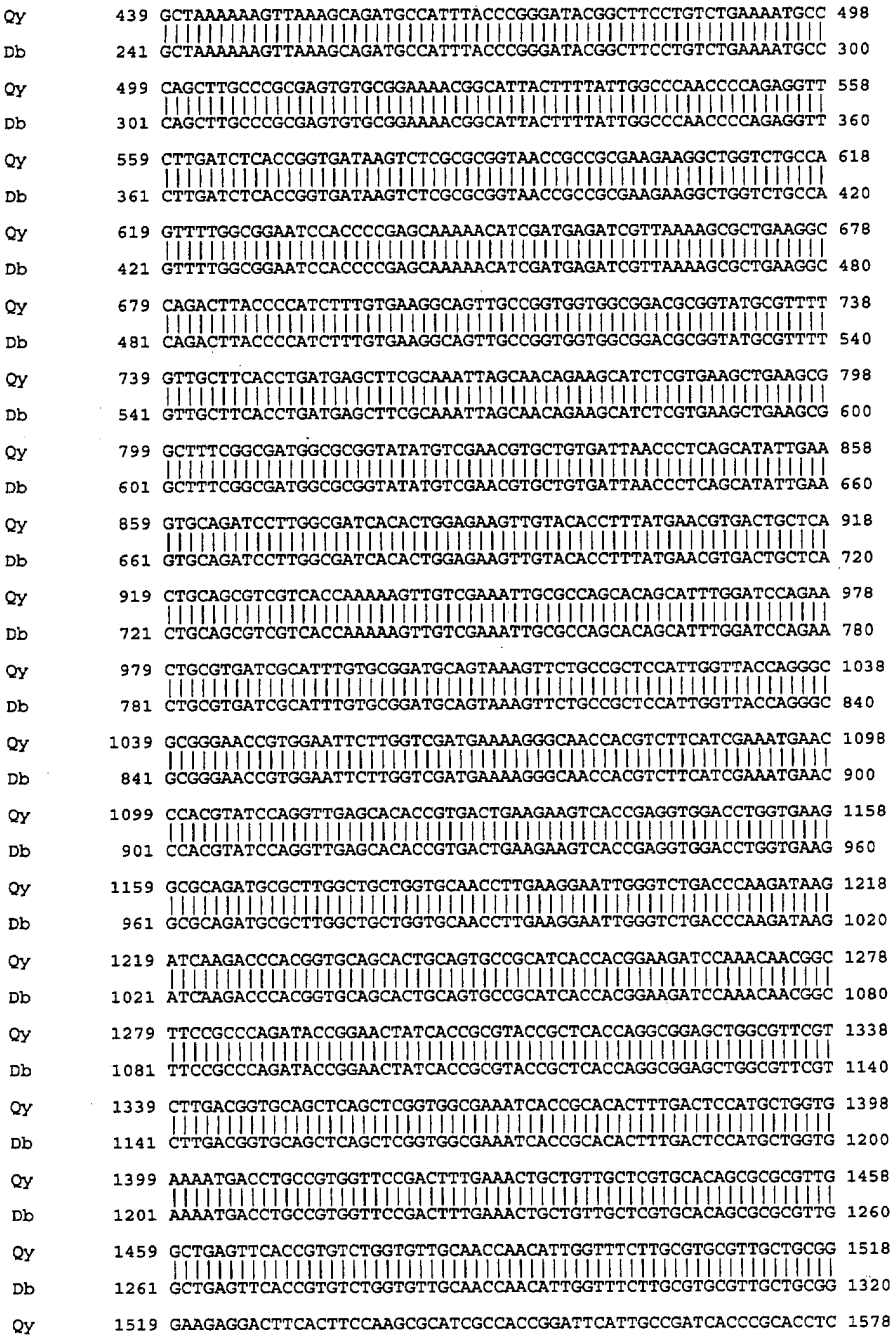
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DEFINITION  Novel polynucleotide.
ACCESSION   BD162966
VERSION     BD162966.1  GI:27868728
KEYWORDS    JP 2002191370-A/765.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3420)
  AUTHORS   Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
  TITLE     Novel polynucleotide
  JOURNAL   Patent: JP 2002191370-A 765 09-JUL-2002;
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            PD   09-JUL-2002
            PF   15-DEC-2000 JP 2000405096
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            PI   HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKIO
            PI   OZAKI
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            PC   C12N5/00,C12N15/00
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ORIGIN

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Qy        199 GTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGC 258
Db          1 GTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGC 60
Qy        259 GGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCT 318
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Qy        319 ATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGC 378
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Qy        499 CAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTT 558
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Qy       1459 GCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGG 1518
Db       1261 GCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGG 1320
Qy       1519 GAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATTGCCGATCACCCGCACCTC 1578
Db       1321 GAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATTGCCGATCACCCGCACCTC 1380
Qy       1579 CTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTC 1638
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DEFINITION  Sequence 1 from Patent WO0231158.
ACCESSION   AX453601
VERSION     AX453601.1  GI:21712841
KEYWORDS    .
SOURCE      Corynebacterium glutamicum
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            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1
  AUTHORS   Hanke,P.D.
  TITLE     Feedback-resistant pyruvate carboxylase gene from corynebacterium
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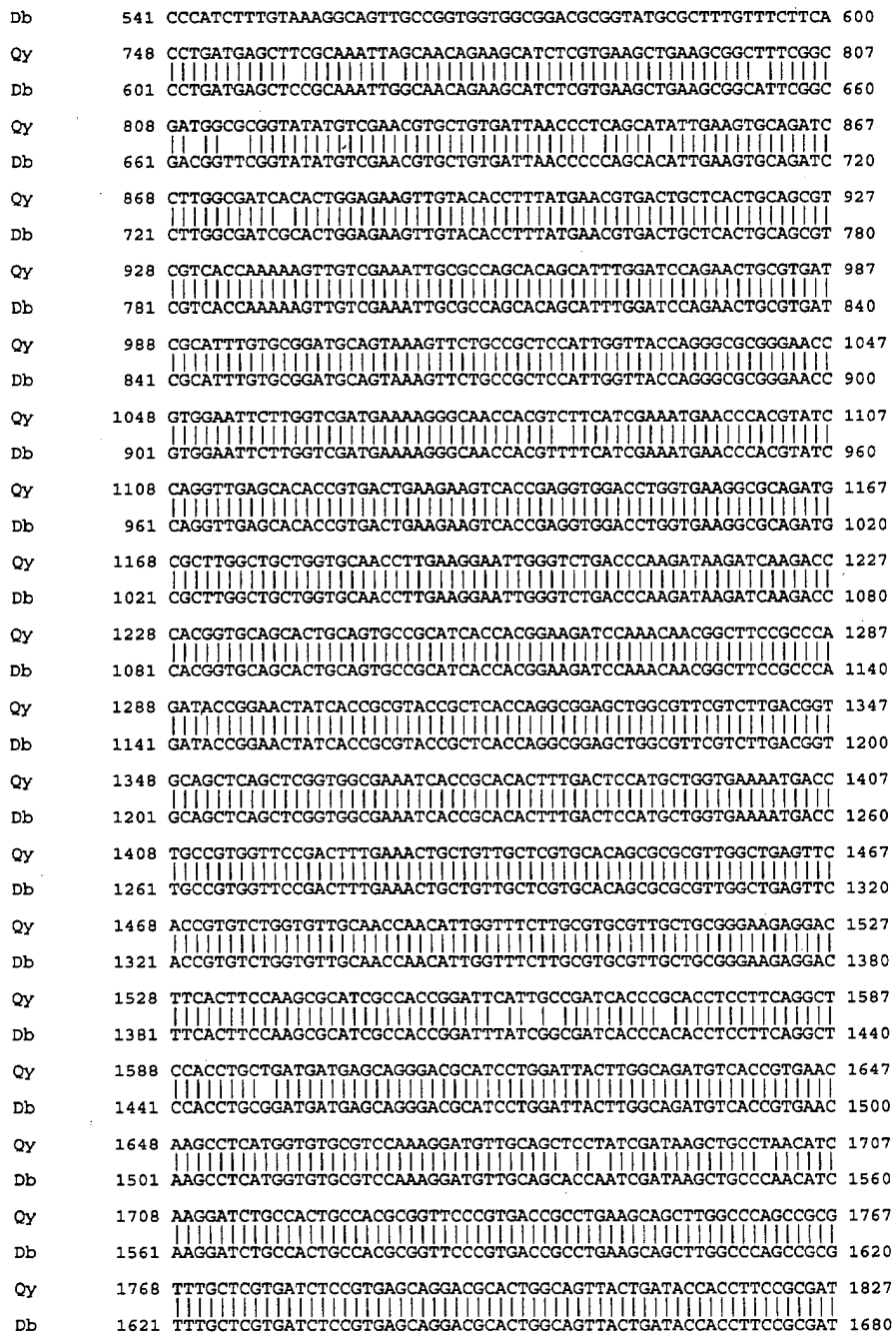

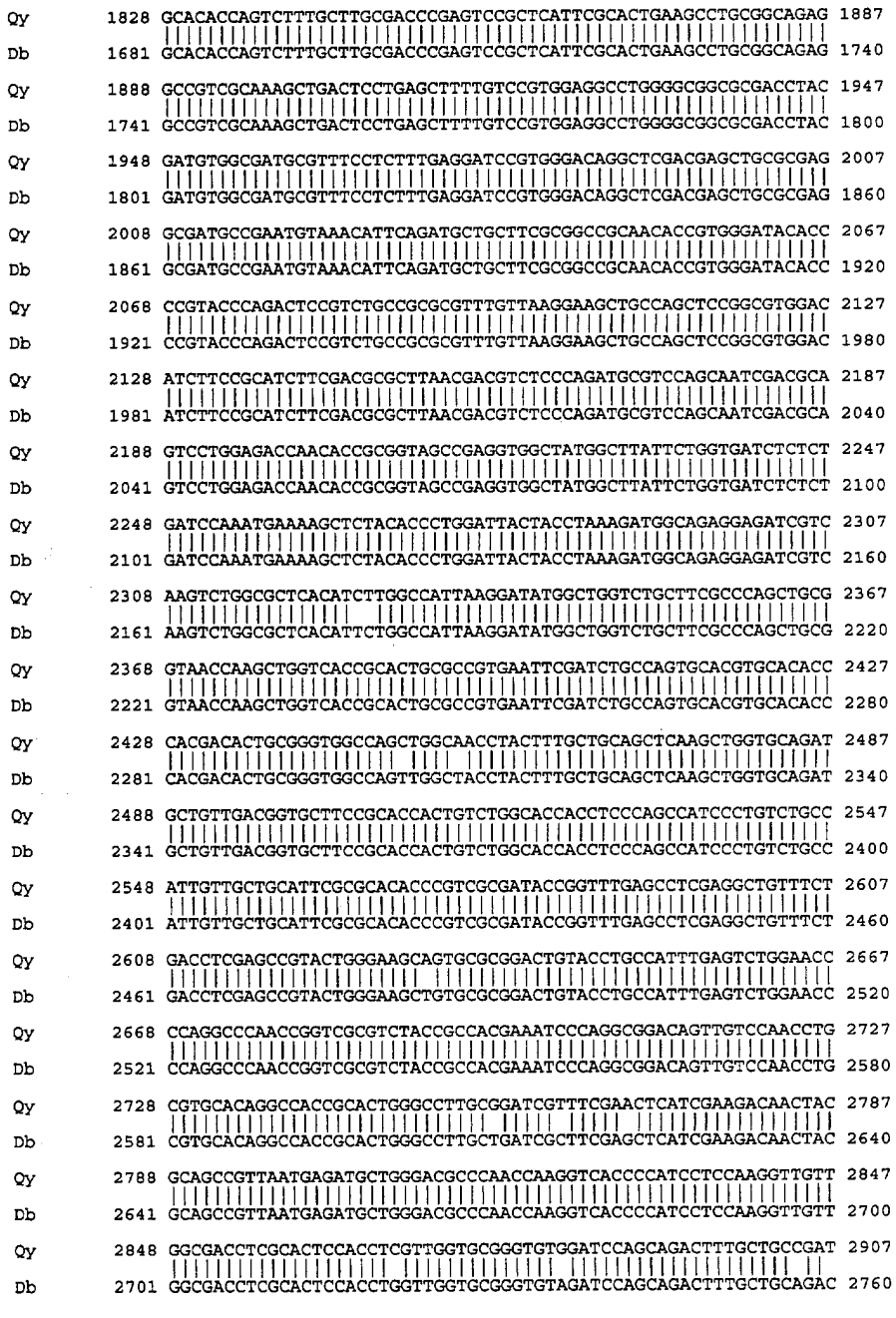

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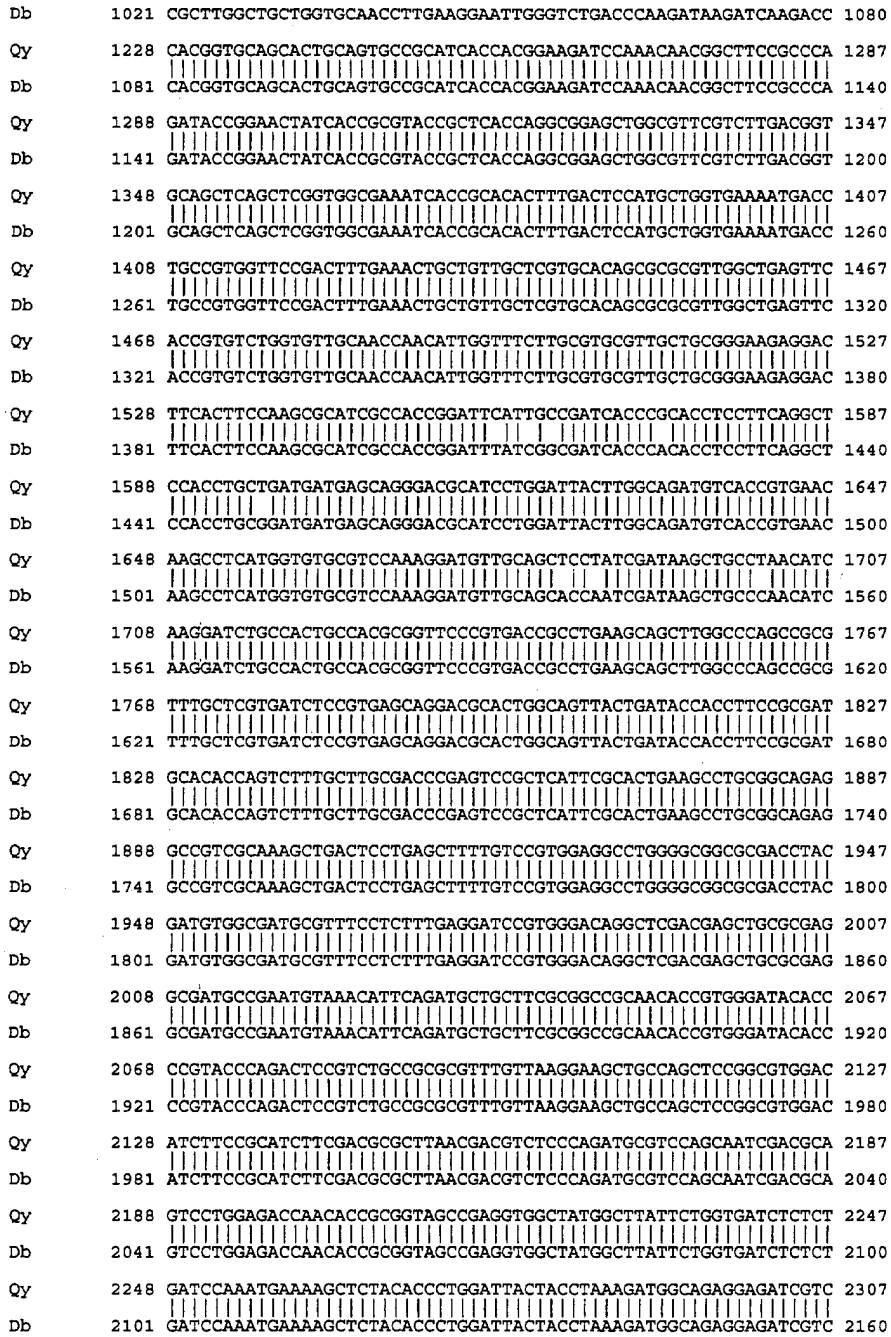
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            Gojobori,T.
  TITLE     Comparative Complete Genome Sequence Analysis of the Amino Acid
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  MEDLINE   22723752
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  AUTHORS   Kawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H. and
            Director-General of Biotechnology Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-2002) Director-General of Biotechnology Center,
            National Institute of Technology and Evaluation, Biotechnology
            Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan
            (E-mail:bio@nite.go.jp, Tel:81-3-3481-1933, Fax:81-3-3481-8424)
COMMENT     Kawarabayasi, Y is officially affiliated with the National
            Institute of Advanced Industrial Science and Technology, Tsukuba,
            Ibaraki, 305-8566 Japan
            Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the
            National Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan
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            Koto-ku, Tokyo, 135-0064 Japan
            Yamagishi, A. is at Tokyo University of Pharmacy and Life Science,
            Hachioji, Tokyo, 192-0392 Japan
            Nishio, Y., Usuda, Y. and Sugimoto, S. are at the Ajinomoto Co.,
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            The other authors are at the National Institute of Technology and
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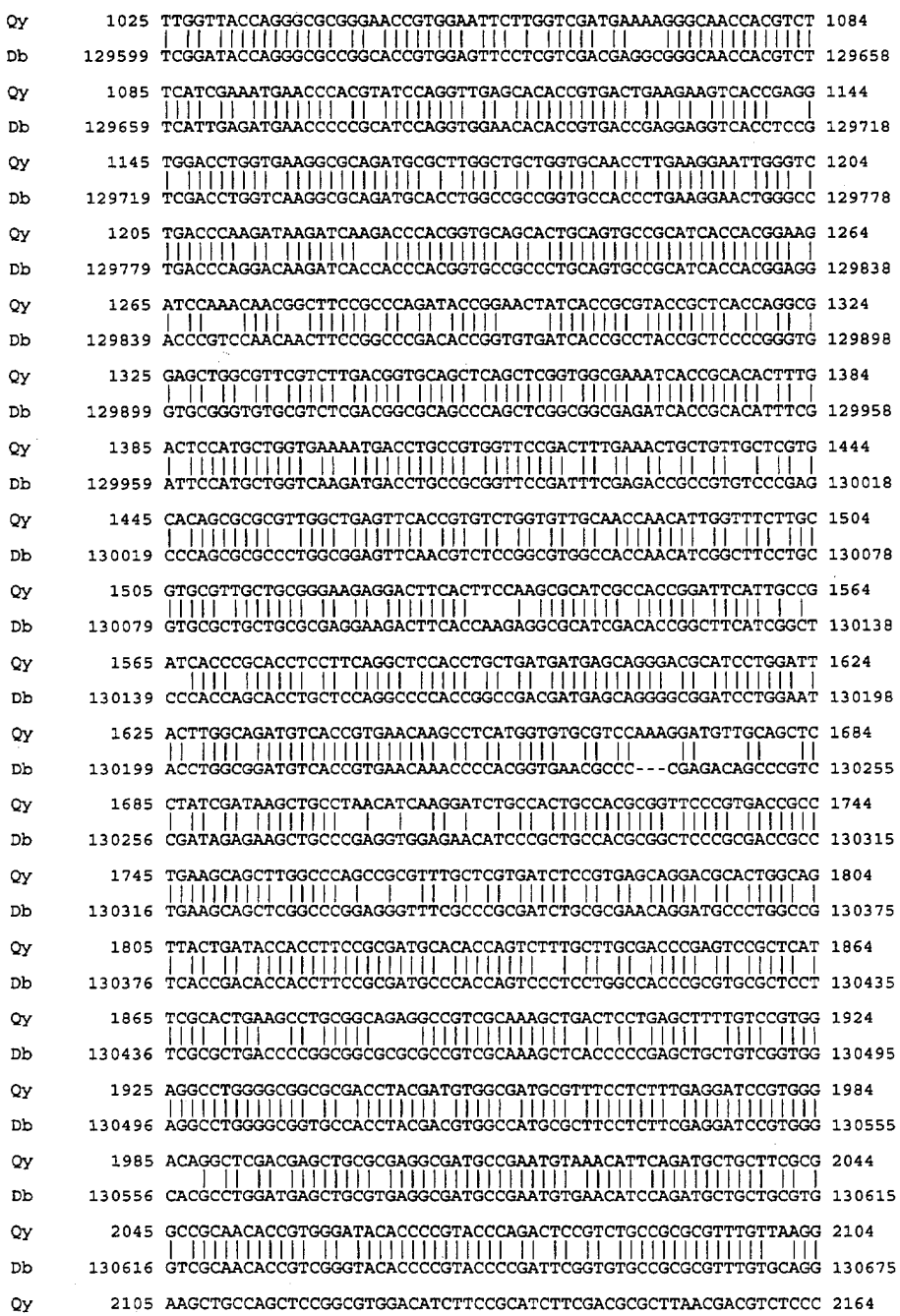
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RESULT 15
BD094153
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DEFINITION  Genes for heat resistant enzymes of amino acid biosynthetic pathway
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ACCESSION   BD094153
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REFERENCE   1  (bases 1 to 4013)
  AUTHORS   Hirano,S., Nonaka,G., Matsuzaki,Y., Akiyoshi,N., Nakamura,K.,
            Kimura,E., Osumi,T., Matsui,K., Kawahara,Y., Kurahashi,O.,
            Nakamatsu,T. and Sugimoto,S.
  TITLE     Genes for heat resistant enzymes of amino acid biosynthetic pathway
            derived from thermophilic coryneform bacteria
  JOURNAL   Patent: WO 0125447-A 11 12-APR-2001;
            AJINOMOTO CO INC,SEIKO HIRANO,GEN NONAKA,YUMI MATSUZAKI, NAOKI
            AKIYOSHI, KANAE NAKAMURA,EIICHIRO KIMURA,TSUYOSHI OSUMI,KAZUHIKO
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            PI   EIICHIRO KIMURA,TSUYOSHI OSUMI,KAZUHIKO
            MATSUI,YOSHIO KAWAHARA,
            PI   OSAMU KURAHASHI,TSUYOSHI NAKAMATSU,SHINICHI SUGIMOTO PC
            C12N15/60,C12N15/54,C12N15/53,C12N15/31,C12N15/56,C12N9/88, PC
            C12N9/12,
            PC   C12N9/04,C07K14/34,C12N9/26,C12N13/04
            CC
            FH   Key             Location/Qualifiers
            FT   CDS             (319). .(3735).
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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ORIGIN

  Query Match           63.0%;  Score 2279.6;  DB 6;  Length 4013;
  Best Local Similarity  77.7%;  Pred. No. 0;
  Matches 2808;  Conservative    0;  Mismatches  799;  Indels    9;  Gaps    4;

Qy          7 GGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGGTCAGGG 66

Db        129 GGGGTCTCGGGCGGGGGGCATTCTTTTCACGGCAAGGTGGTGAAATTCCGCAGGTCACTC 188

Qy         67 GAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGGAATCGG 126

Db        189 CCCGGCCGGCGGTAGAGAACGGAGCGAAAACGGAAAGCAATACGTGGTTTTCCGGACTGG 248

Qy        127 GGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTT--GGCGGTCTCTTGTTGAAAG 184

Db        249 CCGTTACGATGTTCTGAAG-AGTGACTGCCATCACCCAACAGGCTGGTCCTCGTCGAAAG 307

Qy        185 GAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCT 244

Db        308 GAACAAAAACTGTGGTTACAACA---ACACCCTCCACGCTGCCGGCGTTCAAAAAGATCC 364

Qy        245 TGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTG 304

Db        365 TGGTGGCCAACCGAGGTGAAATCGCGGTGCGAGCATTCCGCGCCGCCTACGAGACCGGGG 424

Qy        305 CAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTT 364

Db        425 CCGCAACCGTGGCCATCTACCCCCGGGAGGACCGTGGCTCCTTCCACCGCTCCTTCGCCT 484

Qy        365 CTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATG 424

Db        485 CCGAGGCGGTGAGGATCGGAACCGAGGGCTCACCCGTCAAGGCGTACCTCGATATTGATG 544

Qy        425 AAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCC 484

Db        545 AGATCATCAACGCCGCCAAGAAGGTGAAAGCGGACGCGGTCTACCCGGGGTATGGTTTCC 604

Qy        485 TGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCC 544

Db        605 TTTCGGAAAATGCCCAGCTCGCGCGTGAATGCGCGGAGAACGGCATTACCTTCATCGGTC 664

Qy        545 CAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCGAAGA 604

Db        665 CCACCCCGGAGGTGCTCGACCTCACGGGCGACAAGTCCAAGGCTGTGTCCGCCGCGAAGA 724

Qy        605 AGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATCGTTA 664

Db        725 AGGCCGGGCTGCCGGTGCTGGCGGAATCCACCCCCAGCACCGACATCGATGAGATCGTCA 784

Qy        665 AAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGAC 724

Db        785 AGAGTGCCGAGGGGCAGACCTACCCGATCTTCGTCAAGGCCGTCGCAGGTGGTGGCGGGC 844

Qy        725 GCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTC 784

Db        845 GTGGTATGCGGTTCGTCGAGAAGCCCGAGGACCTGCGTGAGCTGGCCAGGGAGGCCTCCC 904

Qy        785 GTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATTAACC 844

Db        905 GCGAGGCGGAGGCCGCTTTCGGTGACGGATCCGTCTACGTCGAACGGGCCGTGATCAAAC 964

Qy        845 CTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTTTATG 904

Db        965 CCCAGCACATCGAGGTGCAGATCCTCGGTGATCACACCGGCGATGTCATCCACCTGTATG 1024

Qy        905 AACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGC 964

Db       1025 AACGCGACTGTTCCCTGCAGCGCCGCCACCAGAAGGTCGTGGAGATCGCACCTGCCCAGC 1084
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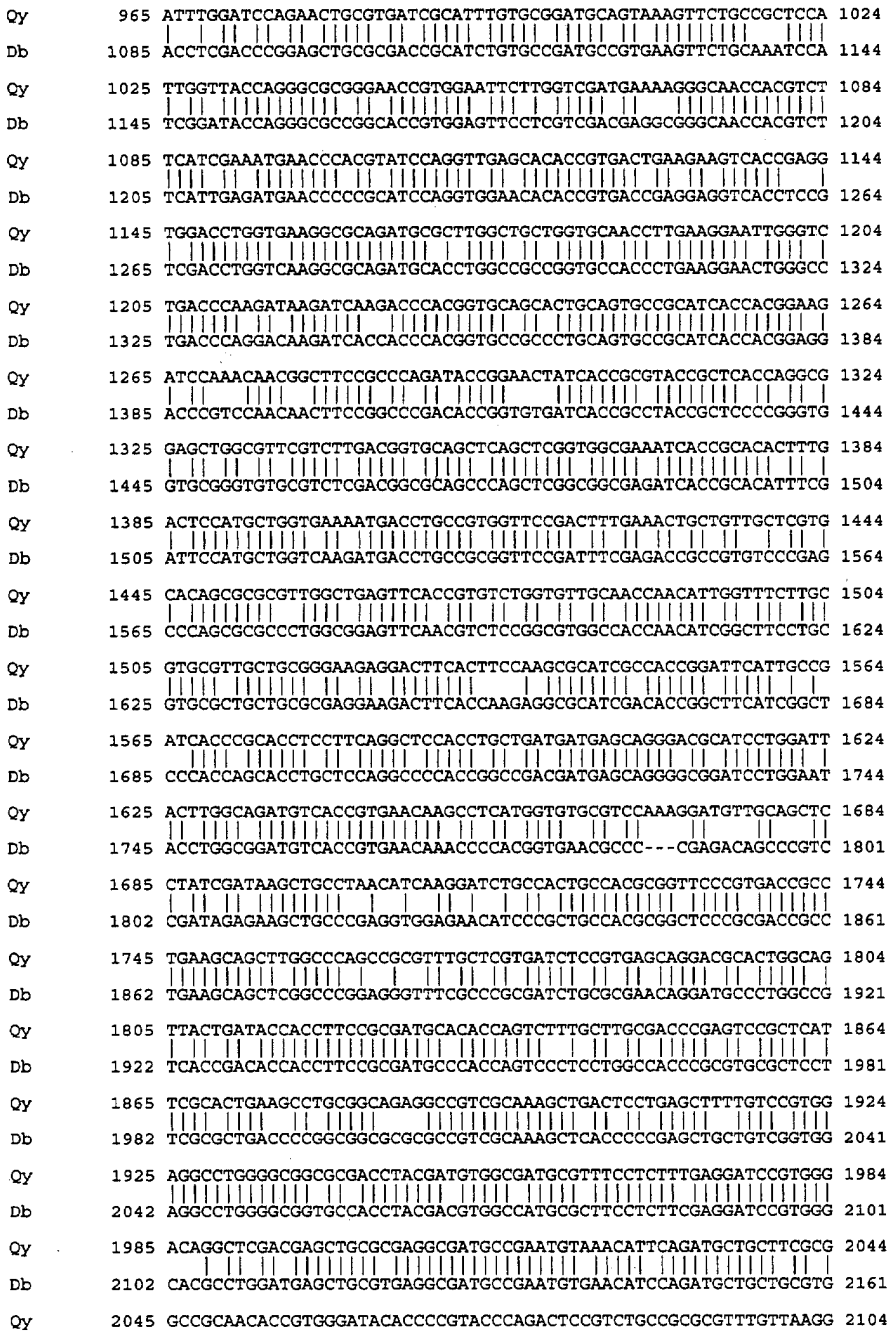

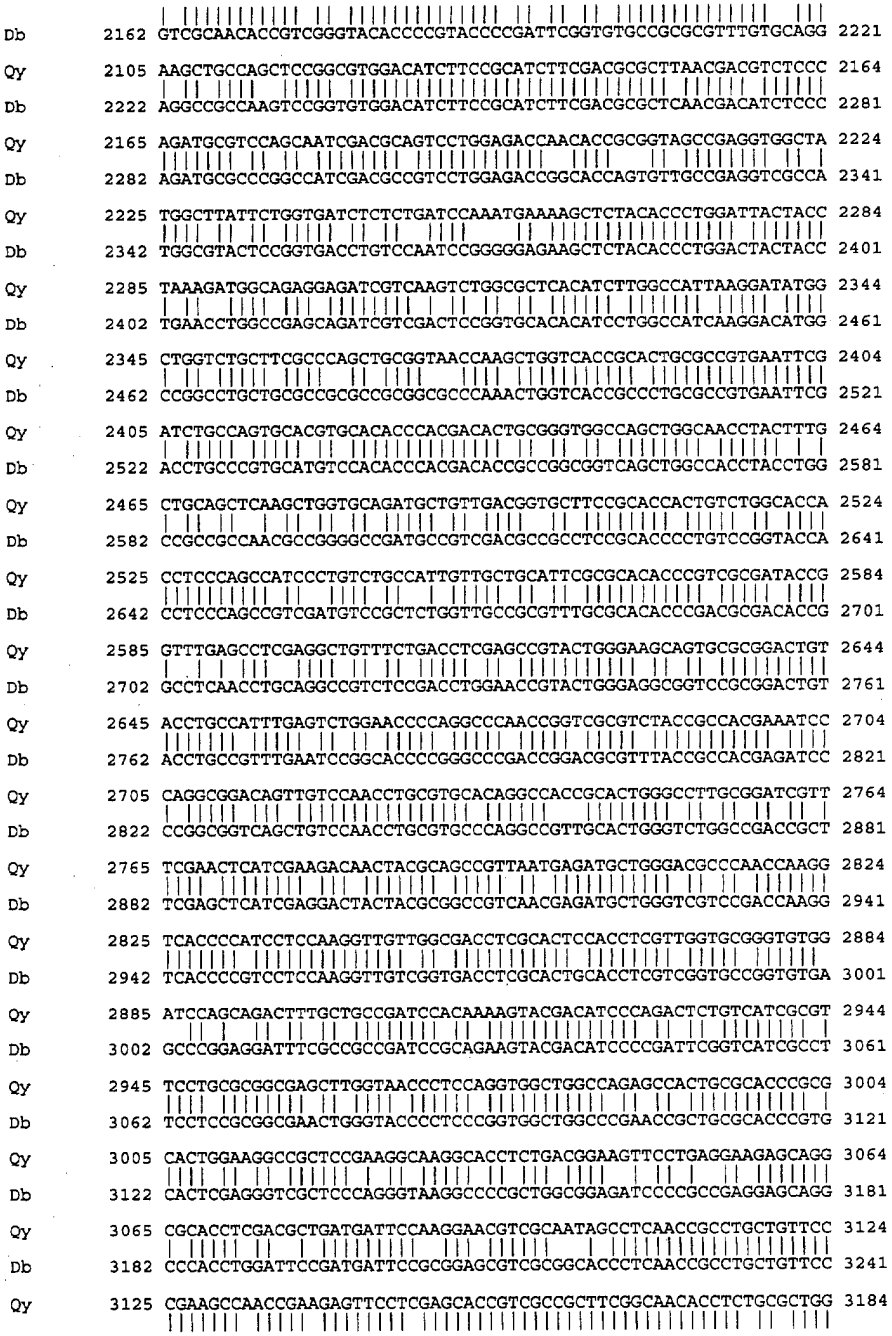

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              |||| || || |||||||||||| ||   || || || |||    ||||||| ||| | |
Db       3302 ATGACCGCGAGTTCTTCTACGGCTTGAAGGAGGGACGTGAGGAGCTGATCCGACTGACCG 3361

Qy       3245 ATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTA 3304
               ||||  ||||||  || | || |||||||||||| | || || || || || || || |
Db       3362 GTGTGTCCACCCCGATGGTGGTCCGCCTGGATGCGGTGTCCGAACCGGATGACAAAGGCA 3421

Qy       3305 TGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCT 3364
              ||||||| || |||| |||||||||||||||||||||||| ||    ||||| ||||| |
Db       3422 TGCGCAACGTGGTGGTCAACGTCAACGGCCAGATCCGCCCGATCAAGGTGCGCGACCGTT 3481

Qy       3365 CCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTG 3424
              |||| ||||| |||||||| ||||| || ||||| ||| || |||||||||||||||| |
Db       3482 CCGTGGAGTCCGTCACCGCCACCGCGGAGAAGGCCGATGCCACCAACAAGGGCCATGTCG 3541

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              | |||||||||||| ||||| |||||||||||| || || || |||||||||| ||||||||||
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              | || || || || ||||| ||||| |||||||||||| || || ||||| ||  |||| |
Db       3602 GCGACGCCGTGGCCATCATTGAGGCCATGAAGATGGAGGCCACCATCACCGCGCCTGTCG 3661

Qy       3545 ACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGA 3604
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Db       3662 ACGGTGTCATCGACCGCGTCGTGGTGCCCGCCGCCACCAAGGTCGAGGGCGGCGACCTCA 3721

Qy       3605 TCGTCGTCGTTTCCTA 3620
              |||| ||||| |||||
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Search completed: March 24, 2004, 00:13:39
Job time : 13746 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 17:20:33 ; Search time 1295 Seconds
(without alignments)
11878.552 Million cell updates/sec

Title: US-10-045-072-1
Perfect score: 3621
Sequence: 1 tggggcggggttagatcctg.....tgatcgtcgtcgtttcctaa 3621

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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6: geneseqn2002s:*
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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3621	100.0	3621	3	AAA47533	Aaa47533 Sequence
	2	3621	100.0	3621	5	AAF32165	Aaf32165 Corynebac
	3	3621	100.0	3621	6	AAD42046	Aad42046 Corynebac
	4	3621	100.0	3621	8	ACA62133	Aca62133 DNA encod
	5	3621	100.0	349980	5	AAH68526	Aah68526 C glutami
	6	3576.4	98.8	3728	2	AAX24102	Aax24102 C. glutam
	7	3420	94.4	3420	5	AAH65730	Aah65730 C glutami
	8	3398.8	93.9	3474	6	ABK52832	Abk52832 Corynebac
	9	2279.6	63.0	4013	5	AAF87437	Aaf87437 Corynebac
	10	1927.4	53.2	3423	7	ACA29831	Aca29831 Prokaryot
	11	1708	47.2	1719	4	AAF71419	Aaf71419 Corynebac
	12	1395	38.5	1406	4	AAF71420	Aaf71420 Corynebac
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	17	1292.2	35.7	3381	7	ACA38630	Aca38630 Prokaryot
	18	1249.6	34.5	32155	9	ADB74252	Adb74252 Mycobacte
	19	1033	28.5	1083	4	AAF71418	Aaf71418 Corynebac
	20	1033	28.5	1083	4	AAF71417	Aaf71417 Corynebac
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	22	907	25.0	939	4	AAF71416	Aaf71416 Corynebac
	23	681	18.8	3945	6	ABK63659	Abk63659 Rat seque
	24	681	18.8	3945	7	ABT41829	Abt41829 Toxicity
	25	681	18.8	3945	9	ADB59092	Adb59092 Toxicity-
	26	681	18.8	3945	9	ADB52590	Adb52590 Primary r
	27	677.4	18.7	4017	6	ABN96532	Abn96532 Gene #303
	28	668.4	18.5	4138	4	ABL19577	Abl19577 Drosophil
	29	668.4	18.5	4308	4	ABL19575	Abl19575 Drosophil
	30	668.4	18.5	4369	4	ABL02789	Abl02789 Drosophil
	31	623.4	17.2	4034	4	ABL20985	Abl20985 Drosophil
	32	598	16.5	4152	6	ABQ70879	Abq70879 Listeria
	33	586	16.2	3468	8	ADB08195	Adb08195 Alloiococ
	34	586	16.2	110000	8	ADB12064_05	Continuation (6 of
	35	582.4	16.1	110000	6	ABA90521_06	Continuation (7 of
	36	577.2	15.9	3441	7	ACA36434	Aca36434 Prokaryot
	37	577.2	15.9	110000	6	ABA03041_10	Continuation (11 o
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	40	565	15.6	110000	6	ABQ67197_09	Continuation (10 o
	41	522	14.4	3444	7	ACA22812	Aca22812 Prokaryot
	42	514	14.2	3429	4	AAS53072	Aas53072 Enterococ
	43	509.2	14.1	3426	7	ACA18474	Aca18474 Prokaryot
c	44	500.4	13.8	20072	2	AAX13026	Aax13026 Enterococ
c	45	500.4	13.8	20072	6	ABS98821	Abs98821 Enterococ

ALIGNMENTS

RESULT 1
AAA47533
ID AAA47533 standard; DNA; 3621 BP.
XX
AC AAA47533;
XX
DT 20-OCT-2000 (first entry)
XX
DE Sequence encoding pyruvate carboxylase of C. glutamicum.
XX
KW Pyruvate carboxylase; expression; amino acid biosynthesis; lysine;
KW glutamic acid; oxaloacetate; fermentation; biosynthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT CDS 199
FT /*tag= a
FT /product= "Pyruvate carboxylase"
FT /transl_except= (pos:199. .202, aa:Met)
XX
PN WO200039305-A1.
XX
PD 06-JUL-2000.
XX
PF 23-DEC-1998; 98WO-US027301.
XX
PR 23-DEC-1998; 98WO-US027301.
XX
PA (SINS/) SINSKEY A J.
PA (LESS/) LESSARD P A.
PA (WILL/) WILLIS L B.
XX
PI Sinskey AJ, Lessard PA, Willis LB;
XX
DR WPI; 2000-465746/40.
DR P-PSDB; AAB01436.
XX
PT Novel polynucleotides encoding Corynebacterium glutamicum pyruvate
PT carboxylase useful for industrial fermentation processes comprises a
PT specific nucleotide sequence.
XX
PS Claim 3; Fig 1; 51pp; English.
XX
CC The pyruvate carboxylase of Corynebacterium glutamicum can be used for
CC producing amino acids, preferably lysine and glutamic acid in industrial

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CC   fermentations and for replenishing oxaloacetate consumed for biosynthesis
CC   during growth. By incorporating the pyruvate carboxylase gene in
CC   expression vectors levels of expression can be 2 - 20 fold higher than in
CC   Corynebacterium glutamicum
XX
SQ   Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 3621;  DB 3;  Length 3621;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3621;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
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Qy         61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120
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Qy        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180
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Qy        181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
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Qy        241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300
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Qy        301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360
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Db        301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360

Qy        361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420
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Qy        421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
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Db        421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480

Qy        481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540
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Db        481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540

Qy        541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600
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Db        541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600

Qy        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660
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Db        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660

Qy        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
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Db        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720

Qy        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
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Db        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780

Qy        781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840

Qy        841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
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Qy        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960
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Qy        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
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Qy       1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080
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Qy       1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
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Qy       1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
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Qy       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
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Qy       1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380
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Qy       1741 CGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTG 1800
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Qy       1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920

Qy       1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980

Qy       1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
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Qy       2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100
Db       2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100

Qy       2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 2160
Db       2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 2160

Qy       2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220
Db       2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220

Qy       2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
Db       2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280

Qy       2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
Db       2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340

Qy       2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
Db       2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400

Qy       2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
Db       2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460

Qy       2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520
Db       2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520

Qy       2521 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 2580
Db       2521 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 2580

Qy       2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 2640
Db       2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 2640

Qy       2641 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 2700
Db       2641 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 2700

Qy       2701 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 2760
Db       2701 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 2760

Qy       2761 CGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACC 2820
Db       2761 CGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACC 2820

Qy       2821 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 2880
Db       2821 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 2880

Qy       2881 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 2940
Db       2881 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 2940

Qy       2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
Db       2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000

Qy       3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060
Db       3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060

Qy       3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120
Db       3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120

Qy       3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180
Db       3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180

Qy       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
Db       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240

Qy       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
Db       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300

Qy       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Db       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360

Qy       3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420
Db       3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420

Qy       3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Db       3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480

Qy       3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Db       3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540

Qy       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
Db       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600

Qy       3601 TTGATCGTCGTCGTTTCCTAA 3621
Db       3601 TTGATCGTCGTCGTTTCCTAA 3621
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RESULT 2
AAF32165
ID AAF32165 standard; DNA; 3621 BP.
XX
AC AAF32165;
XX
DT 12-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum pyruvate carboxylase coding sequence.
XX
KW Pyruvate carboxylase; anaplerotic pathway; industrial fermentation;
KW oxaloacetate; ds.
XX
OS Corynebacterium glutamicum.
XX
PN US6171833-B1.
XX
PD 09-JAN-2001.
XX
PF 23-DEC-1998; 98US-00220081.
XX
PR 23-DEC-1998; 98US-00220081.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Sinskey AJ, Lessard PA, Willis LB;
XX
DR WPI; 2001-122330/13.
DR P-PSDB; AAB67129.
XX
PT Novel nucleic acid encoding pyruvate carboxylase from Corynebacterium
PT glutamicum, for replenishing oxaloacetate consumed during lysine and
PT glutamic acid production in industrial fermentations.
XX
PS Claim 2; Col 23-30; 29pp; English.
XX

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CC   The present invention provides the protein and coding sequences of the
CC   Corynebacterium glutamicum pyruvate carboxylase protein. This is an
CC   enzyme in the anaplerotic pathway. It can be used in the replenishment of
CC   oxaloacetate consumed during lysine and glutamic acid production in
CC   industrial fermentation
XX
SQ   Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 3621;  DB 5;  Length 3621;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3621;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60

Qy         61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120

Qy        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180

Qy        181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240

Qy        241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300

Qy        301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360

Qy        361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420

Qy        421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480

Qy        481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540

Qy        541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600

Qy        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660

Qy        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720

Qy        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780

Qy        781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840

Qy        841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900

Qy        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960

Qy        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020

Qy       1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080

Qy       1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140

Qy       1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200

Qy       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260

Qy       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320

Qy       1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380

Qy       1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440

Qy       1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500

Qy       1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560

Qy       1561 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 1620

Qy       1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680

Qy       1681 GCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740

Qy       1741 CGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTG 1800

Qy       1801 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 1860

Qy       1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920

Qy       1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980

Qy       1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
Qy       2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100
Qy       2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 2160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 2160
Qy       2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220
Qy       2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
Qy       2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
Qy       2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
Qy       2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
Qy       2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520
Qy       2521 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 2580
Qy       2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 2640
Qy       2641 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 2700
Qy       2701 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 2760
Qy       2761 CGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACC 2820
Qy       2821 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 2880
Qy       2881 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 2940
Qy       2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
Qy       3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060
Qy       3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120
Qy       3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180
Qy       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
Qy       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
Qy       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Qy       3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420
Qy       3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Qy       3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Qy       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
Qy       3601 TTGATCGTCGTCGTTTCCTAA 3621
             |||||||||||||||||||||
Db       3601 TTGATCGTCGTCGTTTCCTAA 3621
```

```
RESULT 3
AAD42046
ID   AAD42046 standard; DNA; 3621 BP.
XX
AC   AAD42046;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Corynebacterium glutamicum pyruvate carboxylase DNA.
XX
KW   Pyruvate carboxylase; anaplerotic enzyme; industrial fermentation;
KW   oxaloacetate; growth; enzyme; gene; ds.
XX
OS   Corynebacterium glutamicum.
XX
FH   Key             Location/Qualifiers
FT   CDS             199. .3621
FT                   /*tag=  a
FT                   /product= "Pyruvate carboxylase protein"
FT                   /transl_except= (pos:199. .201, aa:Met)
XX
PN   US6403351-B1.
XX
PD   11-JUN-2002.
XX
PF   03-OCT-2000; 2000US-00677575.
XX
PR   23-DEC-1998;   98US-00220081.
XX
PA   (ARCH ) ARCHER-DANIELS MIDLAND CO.
XX
PI   Sinskey AJ,  Lessard PA,  Willis LB;
XX
DR   WPI; 2002-536037/57.
DR   P-PSDB; AAE25601.
```

XX
PT Novel pyruvate carboxylase polypeptide, useful for replenishing
PT oxaloacetate consumed for biosynthesis during growth, or lysine and
PT glutamic acid production in industrial fermentation.
XX
PS Disclosure; Col 23-30; 28pp; English.
XX
CC The present invention relates to novel pyruvate carboxylase proteins and
CC polynucleotides encoding such proteins. Sequences of the invention are
CC important anaplerotic enzymes for replenishing oxaloacetate consumed for
CC biosynthesis during growth, or lysine and glutamic acid production in
CC industrial fermentation. The present sequence is C. glutamicum pyruvate
CC carboxylase DNA
XX
SQ Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;

Query Match 100.0%; Score 3621; DB 6; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
Db    1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60

Qy   61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120
Db   61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120

Qy  121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180
Db  121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180

Qy  181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
Db  181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240

Qy  241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300
Db  241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300

Qy  301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360
Db  301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360

Qy  361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420
Db  361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420

Qy  421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
Db  421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480

Qy  481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540
Db  481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540

Qy  541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600
Db  541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600

Qy  601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660
Db  601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660

Qy  661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
Db  661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720

Qy  721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
Db  721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780

Qy  781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840
Db  781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840

Qy  841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
Db  841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900

Qy  901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960
Db  901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960

Qy  961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
Db  961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020

Qy 1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080
Db 1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080

Qy 1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
Db 1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140

Qy 1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
Db 1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200

Qy 1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
Db 1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260

Qy 1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
Db 1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320

Qy 1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380
Db 1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380

Qy 1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440
Db 1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440

Qy 1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500
Db 1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500

Qy 1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560
Db 1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560

Qy 1561 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 1620
Db 1561 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 1620

Qy 1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
Db 1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680

Qy 1681 GCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740
Db 1681 GCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740

Qy 1741 CGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTG 1800
Db 1741 CGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTG 1800

Qy 1801 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 1860
Db 1801 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 1860

Qy 1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920
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Db       1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920
Qy       1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
Db       1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
Qy       1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
Db       1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
Qy       2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100
Db       2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100
Qy       2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 2160
Db       2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 2160
Qy       2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220
Db       2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220
Qy       2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
Db       2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
Qy       2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
Db       2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
Qy       2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
Db       2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
Qy       2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
Db       2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
Qy       2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520
Db       2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520
Qy       2521 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 2580
Db       2521 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 2580
Qy       2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 2640
Db       2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 2640
Qy       2641 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 2700
Db       2641 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 2700
Qy       2701 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 2760
Db       2701 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 2760
Qy       2761 CGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACC 2820
Db       2761 CGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACC 2820
Qy       2821 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 2880
Db       2821 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 2880
Qy       2881 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 2940
Db       2881 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 2940
Qy       2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
Db       2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
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Qy       3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060
Db       3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060
Qy       3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120
Db       3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120
Qy       3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180
Db       3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180
Qy       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
Db       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
Qy       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
Db       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
Qy       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Db       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Qy       3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420
Db       3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420
Qy       3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Db       3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Qy       3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Db       3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Qy       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
Db       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
Qy       3601 TTGATCGTCGTCGTTTCCTAA 3621
Db       3601 TTGATCGTCGTCGTTTCCTAA 3621
```

```
RESULT 4
ACA62133
ID   ACA62133 standard; DNA; 3621 BP.
XX
AC   ACA62133;
XX
DT   25-AUG-2003  (first entry)
XX
DE   DNA encoding Corynebacterium glutamicum pyruvate carboxylase.
XX
KW   Pyruvate carboxylase; gene; anaplerotic enzyme; oxaloacetate;
KW   biosynthesis; growth; lysine production; glutamic acid production;
KW   industrial fermentation; gene; ds.
XX
OS   Corynebacterium glutamicum.
XX
FH   Key             Location/Qualifiers
FT   CDS             199. .3621
FT                   /*tag= a
FT                   /product= "Pyruvate carboxylase"
XX
PN   US2003027305-A1.
XX
PD   06-FEB-2003.
XX
PF   15-JAN-2002; 2002US-00045072.
XX
```

PR 23-DEC-1998; 98US-00220081.
PR 03-OCT-2000; 2000US-00677575.
XX
PA (ARCH) ARCHER-DANIELS MIDLAND CO.
XX
PI Sinskey AJ, Lessard PA, Willis LB;
XX
DR WPI; 2003-479542/58.
DR P-PSDB; ABU10426.
XX
PT New pyruvate carboxylase from Corynebacterium glutamicum, useful as an
PT anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis
PT during growth, or for lysine or glutamic acid production in industrial
PT fermentations.
XX
PS Claim 2; Page 12-16; 29pp; English.
XX
CC The invention describes a new isolated pyruvate carboxylase polypeptide
CC having an amino acid sequence at least 95% identical to a sequence
CC comprising 1140 amino acids from Corynebacterium glutamicum, or the
CC complete amino acid sequence encoded by the cosmid clone deposited with
CC the American Type Culture Collection. The polypeptide is useful as an
CC anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis
CC during growth. The polypeptide is also useful for lysine or glutamic acid
CC production in industrial fermentations. This sequence encodes
CC Corynebacterium glutamicum pyruvate carboxylase
XX
SQ Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;

Query Match 100.0%; Score 3621; DB 8; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60

Qy         61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120

Qy        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180

Qy        181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240

Qy        241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300

Qy        301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360

Qy        361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420

Qy        421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480

Qy        481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540

Qy        541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600

Qy        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660

Qy        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720

Qy        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780

Qy        781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840

Qy        841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900

Qy        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960

Qy        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020

Qy       1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080

Qy       1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140

Qy       1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200

Qy       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260

Qy       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320

Qy       1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380

Qy       1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440

Qy       1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500
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Db       1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500

Qy       1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560
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Db       1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560

Qy       1561 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
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Db       1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680

Qy       1681 GCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740
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Db      1681 GCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740
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Qy      1801 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 1860
Db      1801 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 1860
Qy      1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920
Db      1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920
Qy      1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
Db      1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
Qy      1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
Db      1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
Qy      2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100
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Db      2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220
Qy      2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
Db      2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
Qy      2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
Db      2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
Qy      2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
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Qy      2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
Db      2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
Qy      2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520
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Qy      2641 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 2700
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Qy      2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
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Qy      3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060
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Qy      3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120
Db      3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120
Qy      3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180
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Qy      3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
Db      3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
Qy      3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
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Qy      3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420
Db      3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420
Qy      3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Db      3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Qy      3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Db      3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Qy      3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
Db      3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
Qy      3601 TTGATCGTCGTCGTTTCCTAA 3621
Db      3601 TTGATCGTCGTCGTTTCCTAA 3621
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RESULT 5
AAH68526
ID   AAH68526 standard; DNA; 349980 BP.
XX
AC   AAH68526;
XX
DT   26-SEP-2001  (first entry)
XX
DE   C glutamicum coding sequence fragment SEQ ID NO: 7061.
XX
KW   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW   organic acid synthesis; ds.
XX
OS   Corynebacterium glutamicum.
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XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Disclosure; SEQ ID NO 7061; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 349980 BP; 79274 A; 90638 C; 98727 G; 81341 T; 0 U; 0 Other;

Query Match 100.0%; Score 3621; DB 5; Length 349980;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     105013 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 105072

Qy         61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     105073 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 105132

Qy        121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180
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Db     105133 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 105192

Qy        181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
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Db     105193 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 105252

Qy        241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300
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Db     105253 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 105312

Qy        301 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360
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Qy        361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420
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Db     105373 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 105432

Qy        421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
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Db     105433 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 105492

Qy        481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540
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Db     105493 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 105552

Qy        541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600
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Db     105553 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 105612

Qy        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     105613 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 105672

Qy        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
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Db     105673 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 105732

Qy        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
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Db     105733 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 105792

Qy        781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840
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Db     105793 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 105852

Qy        841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
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Db     105853 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 105912

Qy        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960
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Db     105913 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 105972

Qy        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
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Db     105973 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 106032

Qy       1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     106033 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 106092

Qy       1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
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Db     106093 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 106152

Qy       1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
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Db     106153 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 106212

Qy       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
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Db     106213 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 106272

Qy       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
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Qy       1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380
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Db     106333 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 106392

Qy       1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440
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Db     106393 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 106452

Qy       1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500
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Db     106453 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 106512

Qy       1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560
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Qy       1561 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 1620
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Qy       1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
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Qy       1741 CGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTG 1800
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Qy       1801 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 1860
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Qy       1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920
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Qy       1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
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Qy       1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
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Db     106993 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 107052

Qy       2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100
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Db     107053 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 107112

Qy       2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 2160
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Db     107113 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 107172

Qy       2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107173 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 107232

Qy       2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107233 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 107292

Qy       2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107293 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 107352

Qy       2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107353 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 107412

Qy       2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107413 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 107472

Qy       2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107473 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 107532

Qy       2521 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107533 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 107592

Qy       2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 2640
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Qy       2641 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107653 CTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAA 107712

Qy       2701 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107713 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 107772

Qy       2761 CGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACC 2820
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Db     107773 CGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACC 107832

Qy       2821 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107833 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 107892

Qy       2881 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107893 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 107952

Qy       2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107953 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 108012

Qy       3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108013 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 108072

Qy       3061 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108073 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 108132

Qy       3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108133 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 108192

Qy       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108193 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 108252

Qy       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108253 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 108312

Qy       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108313 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 108372

Qy       3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108373 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 108432

Qy       3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108433 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 108492

Qy       3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108493 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 108552

Qy       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108553 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 108612

Qy       3601 TTGATCGTCGTCGTTTCCTAA 3621
             |||||||||||||||||||||
Db     108613 TTGATCGTCGTCGTTTCCTAA 108633
```

RESULT 6
AAX24102
ID AAX24102 standard; DNA; 3728 BP.
XX

```
AC   AAX24102;
XX
DT   30-JUN-1999  (first entry)
XX
DE   C. glutamicum pyruvate carboxylase genomic DNA.
XX
KW   Pyruvate carboxylase; amino acid production; lysine production;
KW   threonine production; homoserine production; glutamate production;
KW   arginine production; feed additive; condiment; pharmaceutical;
KW   fine chemical; ss.
XX
OS   Corynebacterium glutamicum.
XX
FH   Key             Location/Qualifiers
FT   CDS             165. .3587
FT                   /*tag=  a
FT                   /product= "pyruvate carboxylase"
XX
PN   DE19831609-A1.
XX
PD   15-APR-1999.
XX
PF   14-JUL-1998;   98DE-01031609.
XX
PR   04-OCT-1997;   97DE-01043894.
XX
PA   (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI   Peters-Wendisch P,  Eikmanns B,  Sahm H;
XX
DR   WPI; 1999-245521/21.
DR   P-PSDB; AAW93971.
XX
PT   Increasing microbial production of specific amino acids by increasing
PT   activity or expression of pyruvate carboxylase.
XX
PS   Claim 16; Page 8-11; 18pp; German.
XX
CC   This invention describes the isolation of a pyruvate carboxylase from
CC   Corynebacterium glutamicum which is used in a novel method for production
CC   of lysine, threonine, homoserine, glutamate and/or arginine, variously
CC   useful as feed additives, condiments, pharmaceuticals and intermediates
CC   for fine chemicals. Increasing pyruvate carboxylase activity increases
CC   the yield of microbial production of amino acids of the asparate and/or
CC   glutamate families, e.g. about 50% more lysine, 40% more threonine and
CC   150% more homoserine are secreted into the culture medium
XX
SQ   Sequence 3728 BP; 813 A; 1059 C; 1035 G; 821 T; 0 U; 0 Other;

  Query Match             98.8%;  Score 3576.4;  DB 2;  Length 3728;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         44 GCTTGAAGTCGTGCAGGTCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAAC 103
Db         10 GCTTGAAGTCGTGCAGGTCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAAC 69

Qy        104 CGATGTTTGATTGGGGGAATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCC 163
Db         70 CGATGTTTGATTGGGGGAATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCC 129

Qy        164 TTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGC 223
Db        130 TTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGC 189

Qy        224 TTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCC 283
Db        190 TTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCC 249

Qy        284 GTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGAT 343
Db        250 GTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGAT 309

Qy        344 CATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCA 403
Db        310 CATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCA 369

Qy        404 AGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCA 463
Db        370 AGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCA 429

Qy        464 TTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAA 523
Db        430 TTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAA 489

Qy        524 ACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTC 583
Db        490 ACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTC 549

Qy        584 GCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCA 643
Db        550 GCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCA 609

Qy        644 AAAACATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGG 703
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Qy        704 CAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCA 763
Db        670 CAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCA 729

Qy        764 AATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATG 823
Db        730 AATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATG 789

Qy        824 TCGAACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTG 883
Db        790 TCGAACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTG 849

Qy        884 GAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTG 943
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Qy        944 TCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATG 1003
Db        910 TCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATG 969

Qy       1004 CAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCG 1063
Db        970 CAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCG 1029

Qy       1064 ATGAAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCG 1123
Db        1030 ATGAAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCG 1089

Qy       1124 TGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTG 1183
Db        1090 TGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTG 1149

Qy       1184 CAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGC 1243
Db        1150 CAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGC 1209

Qy       1244 AGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCA 1303
Db        1210 AGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCA 1269

Qy       1304 CCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTG 1363
Db        1270 CCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTG 1329

Qy       1364 GCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACT 1423
Db        1330 GCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACT 1389

Qy       1424 TTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTG 1483
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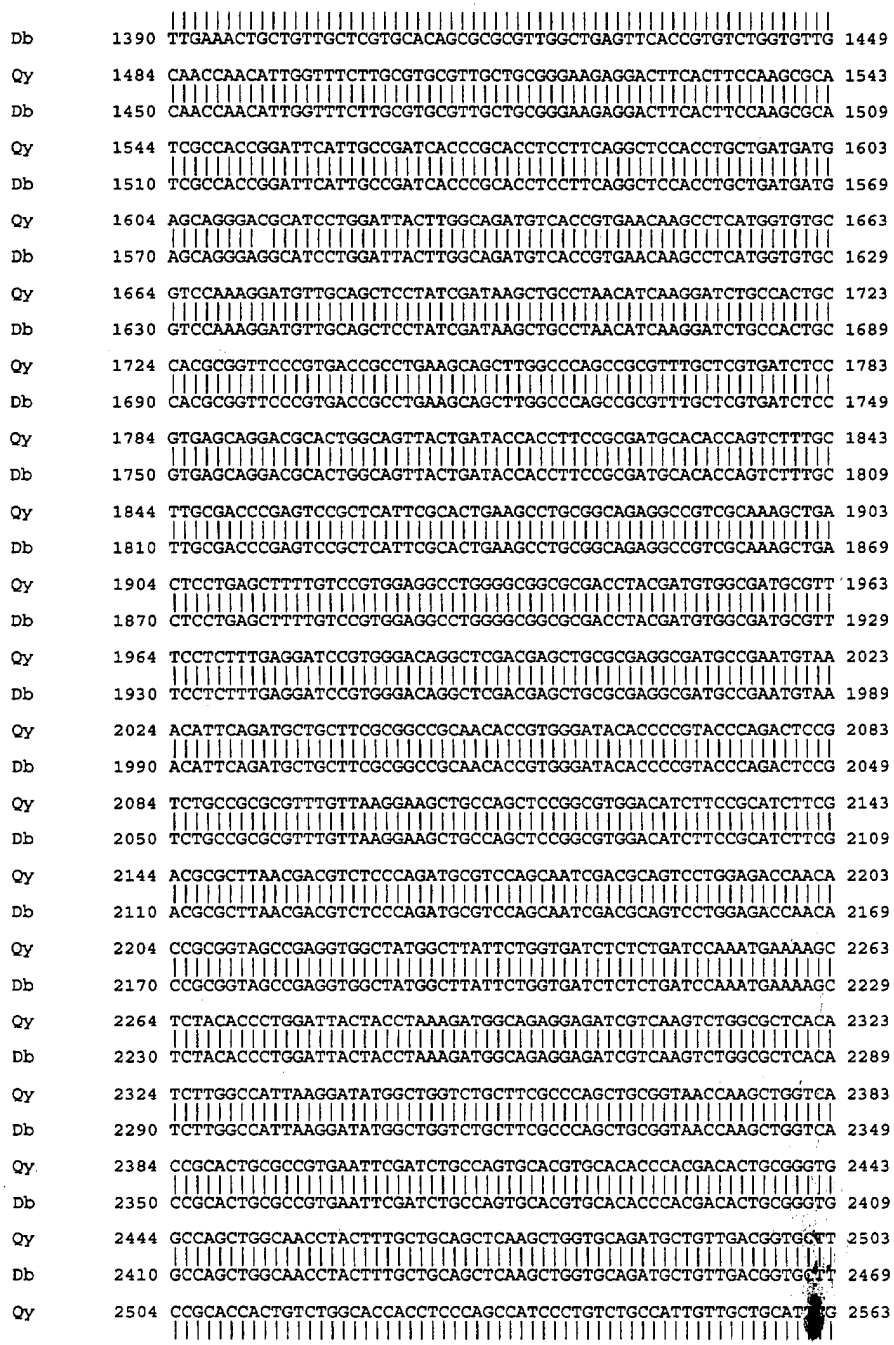
Db 1390 TTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTG 1449
Qy 1484 CAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCA 1543
Db 1450 CAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCA 1509
Qy 1544 TCGCCACCGGATTCATTGCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATG 1603
Db 1510 TCGCCACCGGATTCATTGCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATG 1569
Qy 1604 AGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGC 1663
Db 1570 AGCAGGGAGGCATCCTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGC 1629
Qy 1664 GTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGC 1723
Db 1630 GTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGC 1689
Qy 1724 CACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCC 1783
Db 1690 CACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCC 1749
Qy 1784 GTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGC 1843
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Qy 1844 TTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGA 1903
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Qy 1904 CTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTT 1963
Db 1870 CTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTT 1929
Qy 1964 TCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAA 2023
Db 1930 TCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAA 1989
Qy 2024 ACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCG 2083
Db 1990 ACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCG 2049
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Db 2170 CCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGC 2229
Qy 2264 TCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACA 2323
Db 2230 TCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACA 2289
Qy 2324 TCTTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCA 2383
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Qy 2384 CCGCACTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTG 2443
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Qy 2444 GCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTT 2503
Db 2410 GCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTT 2469
Qy 2504 CCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCG 2563
Db 2470 CCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCG 2529
Qy 2564 CGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACT 2623
Db 2530 CGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACT 2589
Qy 2624 GGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTC 2683
Db 2590 GGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTC 2649
Qy 2684 GCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCG 2743
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Qy 2804 TGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCC 2863
Db 2770 TGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCC 2829
Qy 2864 ACCTCGTTGGTGCGGGTGTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACA 2923
Db 2830 ACCTCGTTGGTGCGGGTGTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACA 2889
Qy 2924 TCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGC 2983
Db 2890 TCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGC 2949
Qy 2984 CAGAGCCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGG 3043
Db 2950 CAGAGCCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGG 3009
Qy 3044 AAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATA 3103
Db 3010 AAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATA 3069
Qy 3104 GCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCT 3163
Db 3070 GCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCT 3129
Qy 3164 TCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCG 3223
Db 3130 TCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCG 3189
Qy 3224 AGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCT 3283
Db 3190 AGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCT 3249
Qy 3284 CTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCC 3343
Db 3250 CTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCC 3309
Qy 3344 CAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATT 3403
Db 3310 CAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATT 3369
Qy 3404 CCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTG 3463
Db 3370 CCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTG 3429
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Qy 3584 AGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA 3621
Db 3550 AGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA 3587

```
RESULT 7
AAH65730
ID   AAH65730 standard; DNA; 3420 BP.
XX
AC   AAH65730;
XX
DT   26-SEP-2001  (first entry)
XX
DE   C glutamicum coding sequence fragment SEQ ID NO: 765.
XX
KW   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW   organic acid synthesis; ds.
XX
OS   Corynebacterium glutamicum.
XX
PN   EP1108790-A2.
XX
PD   20-JUN-2001.
XX
PF   18-DEC-2000; 2000EP-00127688.
XX
PR   16-DEC-1999;   99JP-00377484.
PR   07-APR-2000;  2000JP-00159162.
PR   03-AUG-2000; 2000JP-00280988.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI   Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR   WPI; 2001-376931/40.
DR   P-PSDB; AAG90511.
XX
PT   Novel polynucleotides derived from Coryneform bacteria, for identifying
PT   mutation point of a gene, measuring expression of a gene, analyzing
PT   expression profile or pattern of a gene and identifying homologous gene.
XX
PS   Claim 8; SEQ ID NO 765; 246pp + Sequence Listing; English.
XX
CC   The present invention provides a number of nucleotide and protein
CC   sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC   are useful for identifying the mutation point of a gene derived from a
CC   mutant of coryneform bacterium, measuring expression amount and analysing
CC   the expression profile or expression pattern of a gene derived from
CC   Coryneform bacterium, and identifying a homologue of a gene derived from
CC   coryneform bacterium. Coryneform bacteria are useful for producing amino
CC   acids, nucleic acids, vitamins, saccharides and organic acids,
CC   particularly L-lysine. The present sequence is a nucleic acid described
CC   in the exemplification of the invention. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from the European Patent Office
XX
SQ   Sequence 3420 BP; 732 A; 1004 C; 939 G; 745 T; 0 U; 0 Other;

  Query Match             94.4%;  Score 3420;  DB 5;  Length 3420;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3420;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        199 GTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGC 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGC 60

Qy        259 GGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCT 318
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Qy        319 ATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGC 378
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Qy        379 ATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCA 438
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Qy        439 GCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCC 498
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Db        241 GCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCC 300

Qy        499 CAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTT 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTT 360

Qy        559 CTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCA 420

Qy        619 GTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATCGTTAAAAGCGCTGAAGGC 678
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Qy        679 CAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTT 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        739 GTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCG 798
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Db        541 GTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCG 600

Qy        799 GCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAA 858
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Db        601 GCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAA 660

Qy        859 GTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCA 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        919 CTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAA 978
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Qy        979 CTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGC 1038
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Qy       1039 GCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAAC 1098
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Qy       1399 AAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTG 1458
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Db      1261 GCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGG 1320
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Qy      1579 CTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTC 1638
Db      1381 CTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTC 1440
Qy      1639 ACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTG 1698
Db      1441 ACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTG 1500
Qy      1699 CCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGC 1758
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Qy      1939 GCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAG 1998
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Qy      1999 CTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTG 2058
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Qy      2359 CCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCAC 2418
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Qy      2419 GTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCT 2478
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Qy      2599 GCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAG 2658
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Qy      2659 TCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTG 2718
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Db      2701 GCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAG 2760
Qy      2959 CTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGGCCGC 3018
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Qy      3019 TCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCT 3078
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Qy      3079 GATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAA 3138
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Qy      3139 GAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTC 3198
Db      2941 GAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTC 3000
Qy      3199 TTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCA 3258
Db      3001 TTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCA 3060
Qy      3259 CTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTG 3318
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Qy      3319 GCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTC 3378
Db      3121 GCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTC 3180
Qy      3379 ACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCT 3438
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Qy      3499 ATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAAATCGAT 3558
Db      3301 ATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAAATCGAT 3360
Qy      3559 CGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCC 3618
Db      3361 CGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCC 3420
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RESULT 8
ABK52832
ID ABK52832 standard; DNA; 3474 BP.

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XX
AC   ABK52832;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Corynebacterium glutamicum feedback-resistant pyruvate carboxylase gene.
XX
KW   Feedback-resistant; pyruvate carboxylase enzyme; gene; ds;
KW   aspartic acid feedback inhibition resistant.
XX
OS   Corynebacterium glutamicum.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3474
FT                   /*tag= a
FT                   /product= "Corynebacterium glutamicum feedback-resistant
FT                   pyruvate carboxylase enzyme"
FT                   /transl_except= (pos:1. .3; aa:Met)
XX
PN   WO200231158-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US031893.
XX
PR   13-OCT-2000; 2000US-0239913P.
XX
PA   (ARCH ) ARCHER-DANIELS MIDLAND CO.
XX
PI   Hanke PD;
XX
DR   WPI; 2002-463267/49.
DR   P-PSDB; AAU98050.
XX
PT   Novel mutated, feedback resistant pyruvate carboxylase enzyme
PT   polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine,
PT   L-glycine, L-glutamic acid, L-proline and L-methionine and L-isoleucine.
XX
PS   Claim 3; Fig 1; 42pp; English.
XX
CC   The present invention relates to a new mutated, feedback-resistant
CC   pyruvate carboxylase enzyme. The invention is useful for producing an
CC   amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by
CC   culturing a host cell in a suitable media and separating the amino acid
CC   from the medium. The vector of the invention is useful for replacement of
CC   a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate
CC   carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic
CC   copy of the wild-type pyruvate carboxylase gene with a selectable marker
CC   gene through homologous recombination to form a first recombination
CC   strain, and replacing the selectable marker gene in the first recombinant
CC   strain, with feedback resistant pyruvate carboxylase gene through
CC   homologous recombination to form a second recombinant strain, where the
CC   homologous recombination in the above steps, occurs between the host cell
CC   and the vector. The feedback-resistant pyruvate carboxylase enzyme is
CC   resistant to feedback inhibition from aspartic acid. The present nucleic
CC   acid sequence encodes the feedback-resistant pyruvate carboxylase enzyme
CC   of the invention
XX
SQ   Sequence 3474 BP; 749 A; 1013 C; 950 G; 762 T; 0 U; 0 Other;

  Query Match            93.9%;  Score 3398.8;  DB 6;  Length 3474;
  Best Local Similarity  98.6%;  Pred. No. 0;
  Matches 3427;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy       148 GTGACTGCTATCACCCTTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACT 207
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GTGACTGCTATCACCCTTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACT 60

Qy       208 CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATC 267
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Qy       268 GCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC 327
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Qy       328 CGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACC 387
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Qy       388 GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA 447
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Qy       448 GTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCC 507
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Qy       508 CGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTC 567
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Qy       688 CCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCA 747
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Qy       748 CCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGC 807
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Qy       808 GATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATC 867
            || ||  ||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db       661 GACGGTTCGGTATATGTCGAACGTGCTGTGATTAACCCCCAGCACATTGAAGTGCAGATC 720

Qy       868 CTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 927
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Qy       928 CGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGAT 987
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Qy      1108 CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG 1167
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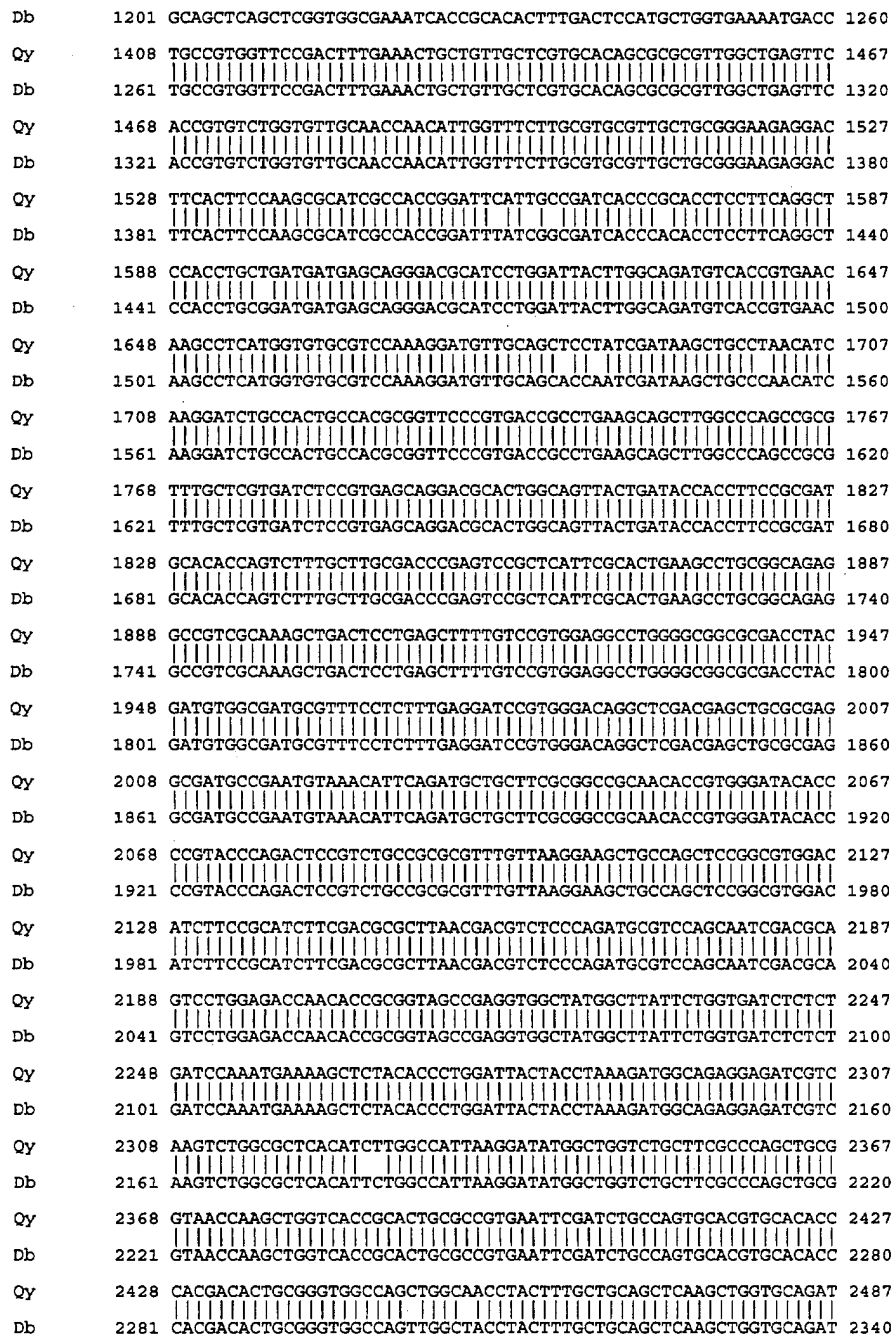
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Db 1261 TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTC 1320
Qy 1468 ACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC 1527
Db 1321 ACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC 1380
Qy 1528 TTCACTTCCAAGCGCATCGCCACCGGATTCATTGCCGATCACCCGCACCTCCTTCAGGCT 1587
Db 1381 TTCACTTCCAAGCGCATCGCCACCGGATTTATCGGCGATCACCCACACCTCCTTCAGGCT 1440
Qy 1588 CCACCTGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC 1647
Db 1441 CCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC 1500
Qy 1648 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATC 1707
Db 1501 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCAATCGATAAGCTGCCCAACATC 1560
Qy 1708 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG 1767
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Db 1621 TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT 1680
Qy 1828 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG 1887
Db 1681 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG 1740
Qy 1888 GCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTAC 1947
Db 1741 GCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTAC 1800
Qy 1948 GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 2007
Db 1801 GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 1860
Qy 2008 GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC 2067
Db 1861 GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC 1920
Qy 2068 CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC 2127
Db 1921 CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC 1980
Qy 2128 ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCA 2187
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Qy 2488 GCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCC 2547
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Qy 2548 ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT 2607
Db 2401 ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT 2460
Qy 2608 GACCTCGAGCCGTACTGGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2667
Db 2461 GACCTCGAGCCGTACTGGGAAGCTGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2520
Qy 2668 CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG 2727
Db 2521 CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG 2580
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Db 2701 GGCGACCTCGCACTCCACCTGGTTGGTGCGGGTGTAGATCCAGCAGACTTTGCTGCAGAC 2760
Qy 2908 CCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAAC 2967
Db 2761 CCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAAC 2820
Qy 2968 CCTCCAGGTGGCTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC 3027
Db 2821 CCTCCAGGTGGCTGGCCAGAACCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC 2880
Qy 3028 AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC 3087
Db 2881 AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC 2940
Qy 3088 AAGGAACGTCGCAATAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTC 3147
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Qy 3148 GAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGC 3207
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Qy 3208 CTGGTCGAAGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT 3267
Db 3061 CTGGTCGAGGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT 3120
Qy 3268 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC 3327
Db 3121 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC 3180
Qy 3328 AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACC 3387
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Qy 3388 GCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTC 3447
Db 3241 GCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTC 3300
Qy 3448 ACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG 3507
Db 3301 ACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG 3360
Qy 3508 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAAATCGATCGCGTTGTG 3567
Db 3361 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATTGAACGCGTTGTG 3420

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Qy       3568 GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA 3621

Db       3421 GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA 3474

RESULT 9
AAF87437
ID   AAF87437 standard; DNA; 4013 BP.
XX
AC   AAF87437;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Corynebacterium thermoaminogenes pc nucleotide sequence.
XX
KW   Corynebacterium; thermophilic; amino acid biosynthesis; enzyme;
KW   thermotolerant; aceA; accBC; dtsR1; dtsR2; pfk; scrB; gluABCD; pdhA; pc;
KW   ppc; acn; icd; lpd; odhA; ds.
XX
OS   Corynebacterium thermoaminogenes.
XX
FH   Key             Location/Qualifiers
FT   CDS             319. .3738
FT                   /*tag=  a
FT                   /product= "pc protein"
XX
PN   WO200125447-A1.
XX
PD   12-APR-2001.
XX
PF   04-OCT-2000; 2000WO-JP006913.
XX
PR   04-OCT-1999;   99JP-00282716.
PR   01-NOV-1999;   99JP-00311147.
PR   21-APR-2000; 2000JP-00120687.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Hirano S,  Nonaka G,  Matsuzaki Y,  Akiyoshi N,  Nakamura K;
PI   Kimura E,  Osumi T,  Matsui K,  Kawahara Y,  Kurahashi O,  Nakamatsu T;
PI   Sugimoto S;
XX
DR   WPI; 2001-300170/31.
DR   P-PSDB; AAB83180.
XX
PT   Proteins and their DNA useful for microbial production of L-amino acids.
XX
PS   Claim 34; Page 126-132; 215pp; Japanese.
XX
CC   The present sequence is provided in a specification relating to genes
CC   encoding thermophilic amino acid biosynthesis system enzymes of the
CC   thermotolerant bacterium Corynebacterium thermoaminogenes. The novel
CC   proteins retain at least 30% isocitrate ligase activity after heating at
CC   50oC for 5 minutes. DNA fragments encoding the enzymes were isolated from
CC   a Corynebacterium thermoaminogenes chromosomal DNA plasmid library by
CC   PCR. The DNA may be used for developing strains of amino acid producing
CC   microorganisms
XX
SQ   Sequence 4013 BP; 735 A; 1376 C; 1234 G; 668 T; 0 U; 0 Other;

  Query Match             63.0%;  Score 2279.6;  DB 5;  Length 4013;
  Best Local Similarity   77.7%;  Pred. No. 0;
  Matches 2808;  Conservative    0;  Mismatches  799;  Indels    9;  Gaps    4;

Qy          7 GGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGGTCAGGG 66

Db        129 GGGGTCTCGGGCGGGGGGCATTCTTTTCACGGCAAGGTGGTGAAATTCCGCAGGTCACTC 188

Qy         67 GAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGGAATCGG 126

Db        189 CCCGGCCGGCGGTAGAGAACGGAGCGAAAACGGAAAGCAATACGTGGTTTTCCGGACTGG 248

Qy        127 GGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTT--GGCGGTCTCTTGTTGAAAG 184

Db        249 CCGTTACGATGTTCTGAAG-AGTGACTGCCATCACCCAACAGGCTGGTCCTCGTCGAAAG 307

Qy        185 GAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCT 244

Db        308 GAACAAAAACTGTGGTTACAACA---ACACCCTCCACGCTGCCGGCGTTCAAAAAGATCC 364

Qy        245 TGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTG 304

Db        365 TGGTGGCCAACCGAGGTGAAATCGCGGTGCGAGCATTCCGCGCCGCCTACGAGACCGGGG 424

Qy        305 CAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTT 364

Db        425 CCGCAACCGTGGCCATCTACCCCCGGGAGGACCGTGGCTCCTTCCACCGCTCCTTCGCCT 484

Qy        365 CTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATG 424

Db        485 CCGAGGCGGTGAGGATCGGAACCGAGGGCTCACCCGTCAAGGCGTACCTCGATATTGATG 544

Qy        425 AAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCC 484

Db        545 AGATCATCAACGCCGCCAAGAAGGTGAAAGCGGACGCGGTCTACCCGGGGTATGGTTTCC 604

Qy        485 TGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCC 544

Db        605 TTTCGGAAAATGCCCAGCTCGCGCGTGAATGCGCGGAGAACGGCATTACCTTCATCGGTC 664

Qy        545 CAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCGAAGA 604

Db        665 CCACCCCGGAGGTGCTCGACCTCACGGGCGACAAGTCCAAGGCTGTGTCCGCCGCGAAGA 724

Qy        605 AGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATCGTTA 664

Db        725 AGGCCGGGCTGCCGGTGCTGGCGGAATCCACCCCCAGCACCGACATCGATGAGATCGTCA 784

Qy        665 AAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGAC 724

Db        785 AGAGTGCCGAGGGGCAGACCTACCCGATCTTCGTCAAGGCCGTCGCAGGTGGTGGCGGGC 844

Qy        725 GCGGTATGCGTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTC 784

Db        845 GTGGTATGCGGTTCGTCGAGAAGCCCGAGGACCTGCGTGAGCTGGCCAGGGAGGCCTCCC 904

Qy        785 GTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATTAACC 844

Db        905 GCGAGGCGGAGGCCGCTTTCGGTGACGGATCCGTCTACGTCGAACGGGCCGTGATCAAAC 964

Qy        845 CTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTTTATG 904

Db        965 CCCAGCACATCGAGGTGCAGATCCTCGGTGATCACACCGGCGATGTCATCCACCTGTATG 1024

Qy        905 AACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGC 964

Db       1025 AACGCGACTGTTCCCTGCAGCGCCGCCACCAGAAGGTCGTGGAGATCGCACCTGCCCAGC 1084

Qy        965 ATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCA 1024

Db       1085 ACCTCGACCCGGAGCTGCGCGACCGCATCTGTGCCGATGCCGTGAAGTTCTGCAAATCCA 1144

Qy       1025 TTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTCT 1084

Db       1145 TCGGATACCAGGGCGCCGGCACCGTGGAGTTCCTCGTCGACGAGGCGGGCAACCACGTCT 1204

Qy       1085 TCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGG 1144

Db       1205 TCATTGAGATGAACCCCCGCATCCAGGTGGAACACACCGTGACCGAGGAGGTCACCTCCG 1264

Qy       1145 TGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTC 1204

Db       1265 TCGACCTGGTCAAGGCGCAGATGCACCTGGCCGCCGGTGCCACCCTGAAGGAACTGGGCC 1324

Qy       1205 TGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAG 1264
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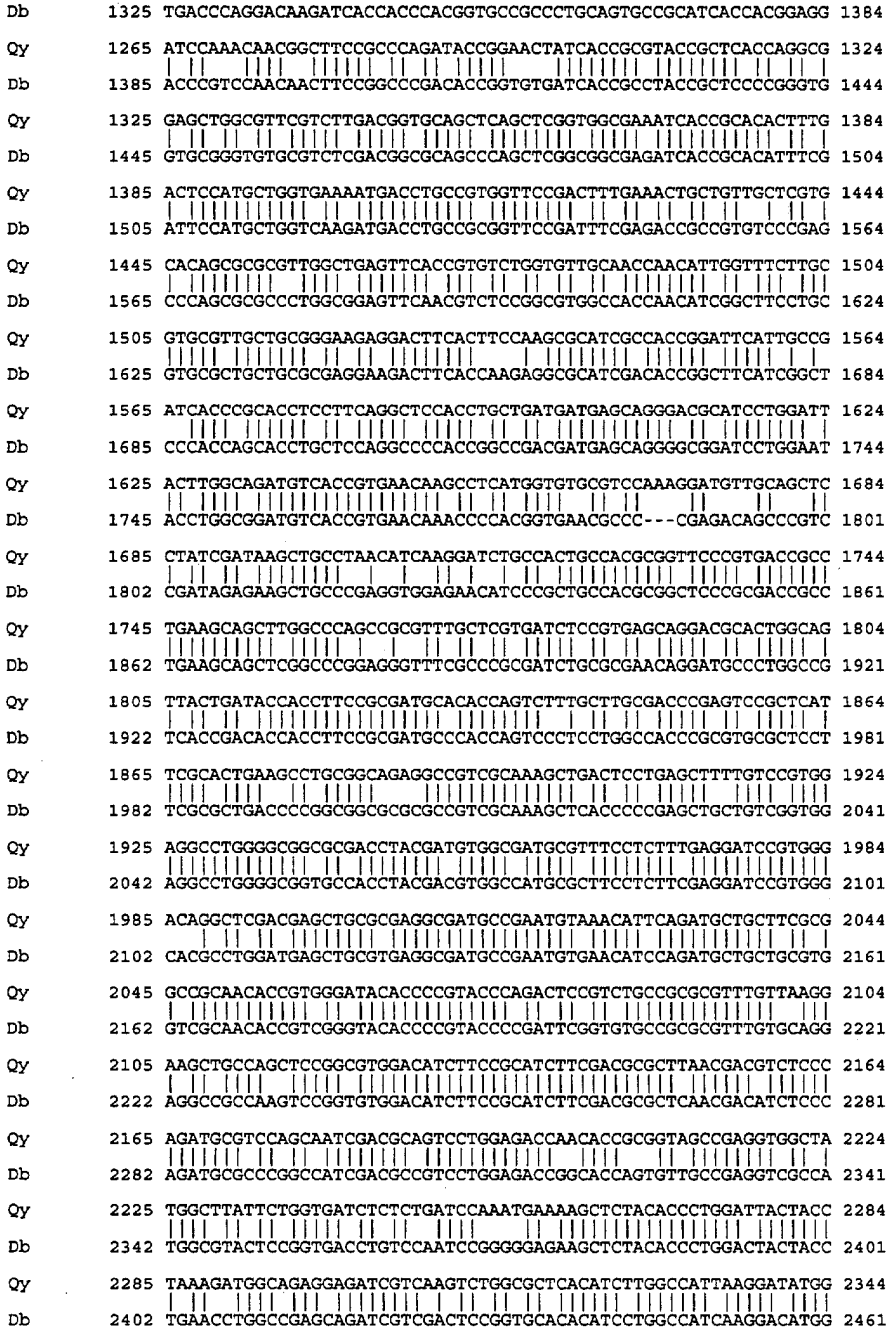
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Qy 1445 CACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGC 1504
Db 1565 CCCAGCGCGCCCTGGCGGAGTTCAACGTCTCCGGCGTGGCCACCAACATCGGCTTCCTGC 1624
Qy 1505 GTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATTGCCG 1564
Db 1625 GTGCGCTGCTGCGCGAGGAAGACTTCACCAAGAGGCGCATCGACACCGGCTTCATCGGCT 1684
Qy 1565 ATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTGGATT 1624
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Db 1922 TCACCGACACCACCTTCCGCGATGCCCACCAGTCCCTCCTGGCCACCCGCGTGCGCTCCT 1981
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Db 1982 TCGCGCTGACCCCGGCGGCGCGCGCCGTCGCAAAGCTCACCCCCGAGCTGCTGTCGGTGG 2041
Qy 1925 AGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGG 1984
Db 2042 AGGCCTGGGGCGGTGCCACCTACGACGTGGCCATGCGCTTCCTCTTCGAGGATCCGTGGG 2101
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Qy 2405 ATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTG 2464
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Qy 2465 CTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCA 2524
Db 2582 CCGCCGCCAACGCCGGGGCCGATGCCGTCGACGCCGCCTCCGCACCCCTGTCCGGTACCA 2641
Qy 2525 CCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCG 2584
Db 2642 CCTCCCAGCCGTCGATGTCCGCTCTGGTTGCCGCGTTTGCGCACACCCGACGCGACACCG 2701
Qy 2585 GTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGACTGT 2644
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Qy       3425 CTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTG 3484
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Qy       3485 GAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTG 3544
             | || || || || ||||| ||||| |||||||||||| || || ||||| ||  |||| |
Db       3602 GCGACGCCGTGGCCATCATTGAGGCCATGAAGATGGAGGCCACCATCACCGCGCCTGTCG 3661

Qy       3545 ACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGA 3604
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Db       3662 ACGGTGTCATCGACCGCGTCGTGGTGCCCGCCGCCACCAAGGTCGAGGGCGGCGACCTCA 3721

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Db       3722 TCGTGGTCGTGTCCTA 3737
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RESULT 10
ACA29831

ID ACA29831 standard; DNA; 3423 BP.
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AC ACA29831;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #11488.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Corynebacterium diphtheriae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU25961.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 17701; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3423 BP; 773 A; 1058 C; 912 G; 680 T; 0 U; 0 Other;

Query Match 53.2%; Score 1927.4; DB 7; Length 3423;
Best Local Similarity 73.4%; Pred. No. 0;
Matches 2494; Conservative 0; Mismatches 896; Indels 9; Gaps 2;

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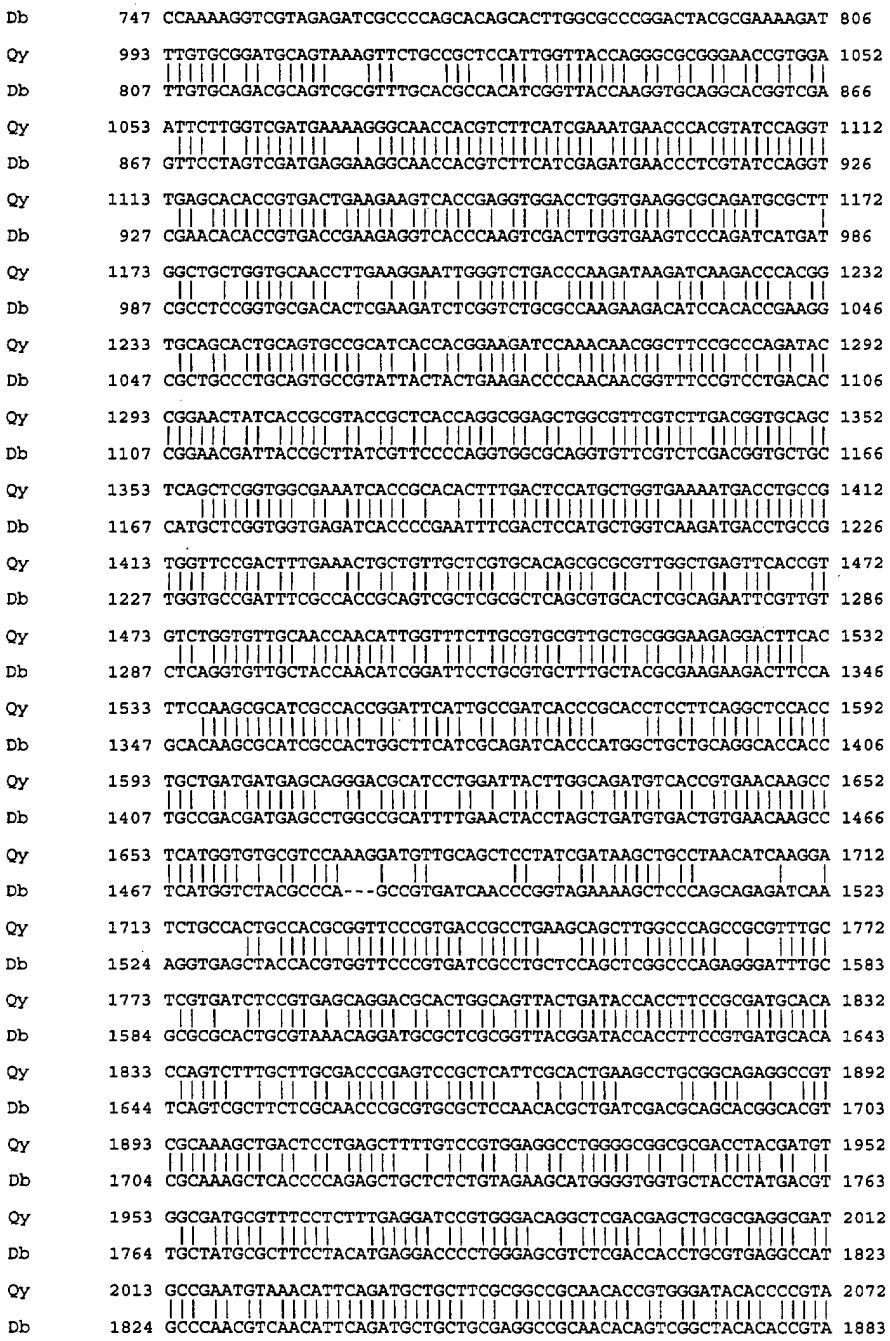
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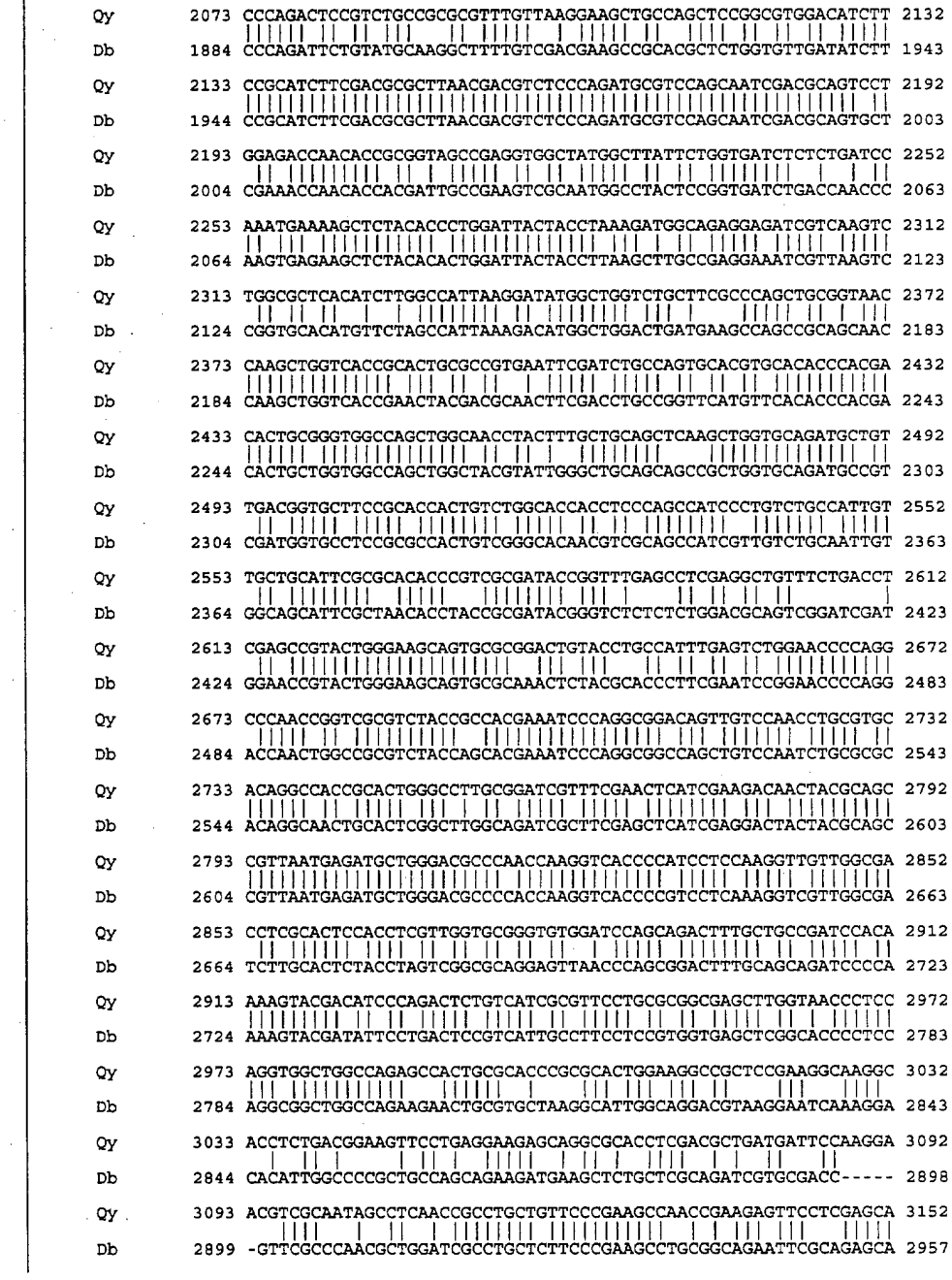
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RESULT 11
AAF71419
ID AAF71419 standard; DNA; 1719 BP.
XX
AC AAF71419;
XX
DT 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:119.
XX
KW Corynebacterium glutamicum; carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
XX
OS Corynebacterium glutamicum.
XX
PN WO200100844-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB000943.
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PR 25-JUN-1999; 99US-0141031P.
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PA (BADI) BASF AG.
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DR WPI; 2001-061975/07.
DR P-PSDB; AAB79302.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
PT metabolism and oxidative phosphorylation protein for production or
PT modulation of production of fine chemicals e.g. amino acids,
PT carbohydrates or enzymes.
XX
PS Claim 3; Page 316-319; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C. glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of
CC fine chemicals, such as, an organic acid, a proteinogenic or
CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
CC encoded by them are used for diagnosing the presence or activity of
CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
CC containing them are used to map genomes of organisms related to C.
CC glutamicum, identify and localise C. glutamicum sequences of interest, in
CC evolutionary studies, in determining SMP protein regions required for
CC function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH)
XX
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Query Match 47.2%; Score 1708; DB 4; Length 1719;
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Db       1021 AAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGAC 1080
Qy       1128 TGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAAC 1187
Db       1081 TGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAAC 1140
Qy       1188 CTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTG 1247
Db       1141 CTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTG 1200
Qy       1248 CCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGC 1307
Db       1201 CCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGC 1260
Qy       1308 GTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGA 1367
Db       1261 GTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGA 1320
Qy       1368 AATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGA 1427
Db       1321 AATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGA 1380
Qy       1428 AACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAAC 1487
Db       1381 AACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAAC 1440
Qy       1488 CAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGC 1547
Db       1441 CAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGC 1500
Qy       1548 CACCGGATTCATTGCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCA 1607
Db       1501 CACCGGATTCATTGCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCA 1560
Qy       1608 GGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCC 1667
Db       1561 GGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCC 1620
Qy       1668 AAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACG 1727
Db       1621 AAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACG 1680
Qy       1728 CGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG 1767
Db       1681 CGGTTCCCGTGACCG-CTGAAGCAGCTTGGCCCAGCCGCG 1719
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RESULT 12
AAF71420
ID AAF71420 standard; DNA; 1406 BP.
XX
AC AAF71420;
XX
DT 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:121.
XX
KW Corynebacterium glutamicum; carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
XX
OS Corynebacterium glutamicum.
XX
PN WO200100844-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB000943.
XX
PR 25-JUN-1999; 99US-0141031P.
PR 08-JUL-1999; 99DE-01031412.
PR 08-JUL-1999; 99DE-01031413.
PR 08-JUL-1999; 99DE-01031419.
PR 08-JUL-1999; 99DE-01031420.
PR 08-JUL-1999; 99DE-01031424.
PR 08-JUL-1999; 99DE-01031428.
PR 08-JUL-1999; 99DE-01031431.
PR 08-JUL-1999; 99DE-01031433.
PR 08-JUL-1999; 99DE-01031434.
PR 08-JUL-1999; 99DE-01031510.
PR 08-JUL-1999; 99DE-01031562.
PR 08-JUL-1999; 99DE-01031634.
PR 09-JUL-1999; 99DE-01032180.
PR 09-JUL-1999; 99DE-01032227.
PR 09-JUL-1999; 99DE-01032230.
PR 09-JUL-1999; 99US-0143208P.
PR 14-JUL-1999; 99DE-01032924.
PR 14-JUL-1999; 99DE-01032973.
PR 14-JUL-1999; 99DE-01033005.

PR 27-AUG-1999; 99DE-01040765.
PR 31-AUG-1999; 99US-0151572P.
PR 03-SEP-1999; 99DE-01042076.
PR 03-SEP-1999; 99DE-01042079.
PR 03-SEP-1999; 99DE-01042086.
PR 03-SEP-1999; 99DE-01042087.
PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042095.
PR 03-SEP-1999; 99DE-01042123.
PR 03-SEP-1999; 99DE-01042125.
XX
PA (BADI) BASF AG.
XX
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX
DR WPI; 2001-061975/07.
DR P-PSDB; AAB79303.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
PT metabolism and oxidative phosphorylation protein for production or
PT modulation of production of fine chemicals e.g. amino acids,
PT carbohydrates or enzymes.
XX
PS Claim 3; Page 321-323; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C. glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of
CC fine chemicals, such as, an organic acid, a proteinogenic or
CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
CC encoded by them are used for diagnosing the presence or activity of
CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
CC containing them are used to map genomes of organisms related to C.
CC glutamicum, identify and localise C. glutamicum sequences of interest, in
CC evolutionary studies, in determining SMP protein regions required for
CC function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH)
XX
SQ Sequence 1406 BP; 325 A; 381 C; 385 G; 315 T; 0 U; 0 Other;

Query Match 38.5%; Score 1395; DB 4; Length 1406;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1406; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy        361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420
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Db          1 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 60

Qy        421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
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Db         61 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 120

Qy        481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 180

Qy        541 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 600
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Db        181 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 240

Qy        601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 300

Qy        661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 360

Qy        721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
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Db        361 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 420

Qy        781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840
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Db        421 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 480

Qy        841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
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Db        481 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 540

Qy        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960
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Db        541 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 600

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Db        721 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 780

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Db        781 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 840

Qy       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
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Db        841 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 900

Qy       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 960

Qy       1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380
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Db        961 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1020

Qy       1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440
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Db       1021 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1080

Qy       1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500
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Db       1081 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1140

Qy       1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560
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Db       1141 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1200

Qy       1561 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 1620
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Qy       1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
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RESULT 13
ACA37896
ID   ACA37896 standard; DNA; 3381 BP.
XX
AC   ACA37896;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #19553.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Mycobacterium avium.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU34026.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 25766; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 3381 BP; 542 A; 1154 C; 1196 G; 489 T; 0 U; 0 Other;

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  Best Local Similarity  63.2%;  Pred. No. 0;
  Matches 2131;  Conservative    0;  Mismatches 1234;  Indels    9;  Gaps    2;

Qy       238 AAGATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAA 297
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Qy       298 ACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCT 357
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Qy       358 TTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGAC 417
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Qy       478 GGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTT 537
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Qy       538 ATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCC 597
Db       310 GTCGGCCCCAGCGCCGAGGTGCTCGAGCTCACCGGCGACAAGTCGCGGGCCATCGCGGCG 369

Qy       598 GCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAG 657
Db       370 GCGCGGGCCGCGGGTCTTCCGGTGCTGGCCTCCTCGCCGCCGTCGACCTCGGTGCAGGAG 429

Qy       658 ATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGT 717
Db       430 TTGCTGAGCGCCGCCGAGACGATGACGTTCCCGCTGTTCGTCAAGGCGGTCGCCGGCGGC 489

Qy       718 GGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAA 777
Db       490 GGCGGCCGGGGGATGCGCCGGGTCACCGATCCGGGGGCGCTGGCCGAGGCGATCGAGGCG 549

Qy       778 GCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTG 837
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Qy       838 ATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACAC 897
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Qy       898 CTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCA 957
Db       670 CTCTACGAGCGGGACTGCAGCGTGCAGCGCCGGCACCAGAAGGTGATCGAGATCGCCCCG 729

Qy       958 GCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGC 1017
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Qy      1018 CGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAAC 1077
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Db       910 ACCGACGTCGACCTGGTGTCCGCGCAGCTGCGCATCGCCTCCGGCCAGACGCTGGAAGAG 969

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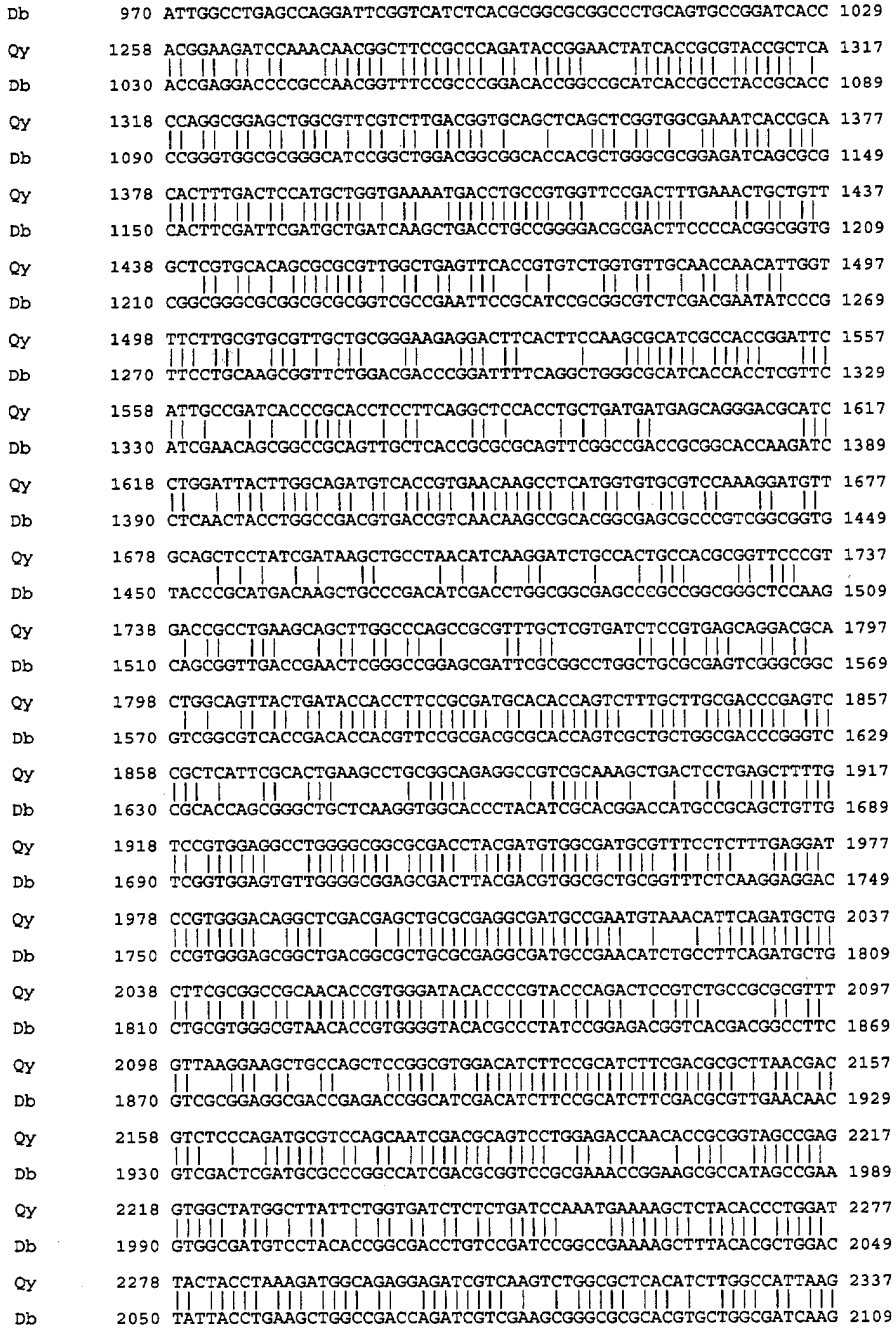
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Qy 1318 CCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCA 1377
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Qy 1378 CACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTT 1437
Db 1150 CACTTCGATTCGATGCTGATCAAGCTGACCTGCCGGGGACGCGACTTCCCCACGGCGGTG 1209
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Db 1210 CGGCGGGCGCGGCGCGCGGTCGCCGAATTCCGCATCCGCGGCGTCTCGACGAATATCCCG 1269
Qy 1498 TTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTC 1557
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Qy 1558 ATTGCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATC 1617
Db 1330 ATCGAACAGCGGCCGCAGTTGCTCACCGCGCGCAGTTCGGCCGACCGCGGCACCAAGATC 1389
Qy 1618 CTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTT 1677
Db 1390 CTCAACTACCTGGCCGACGTGACCGTCAACAAGCCGCACGGCGAGCGCCCGTCGGCGGTG 1449
Qy 1678 GCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGT 1737
Db 1450 TACCCGCATGACAAGCTGCCCGACATCGACCTGGCGGCGAGCCCGCCGGCGGGCTCCAAG 1509
Qy 1738 GACCGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCA 1797
Db 1510 CAGCGGTTGACCGAACTCGGGCCGGAGCGATTCGCGGCCTGGCTGCGCGAGTCGGGCGGC 1569
Qy 1798 CTGGCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTC 1857
Db 1570 GTCGGCGTCACCGACACCACGTTCCGCGACGCGCACCAGTCGCTGCTGGCGACCCGGGTC 1629
Qy 1858 CGCTCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTG 1917
Db 1630 CGCACCAGCGGGCTGCTCAAGGTGGCACCCTACATCGCACGGACCATGCCGCAGCTGTTG 1689
Qy 1918 TCCGTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGAT 1977
Db 1690 TCGGTGGAGTGTTGGGGCGGAGCGACTTACGACGTGGCGCTGCGGTTTCTCAAGGAGGAC 1749
Qy 1978 CCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTG 2037
Db 1750 CCGTGGGAGCGGCTGACGGCGCTGCGCGAGGCGATGCCGAACATCTGCCTTCAGATGCTG 1809
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Qy 2158 GTCTCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAG 2217
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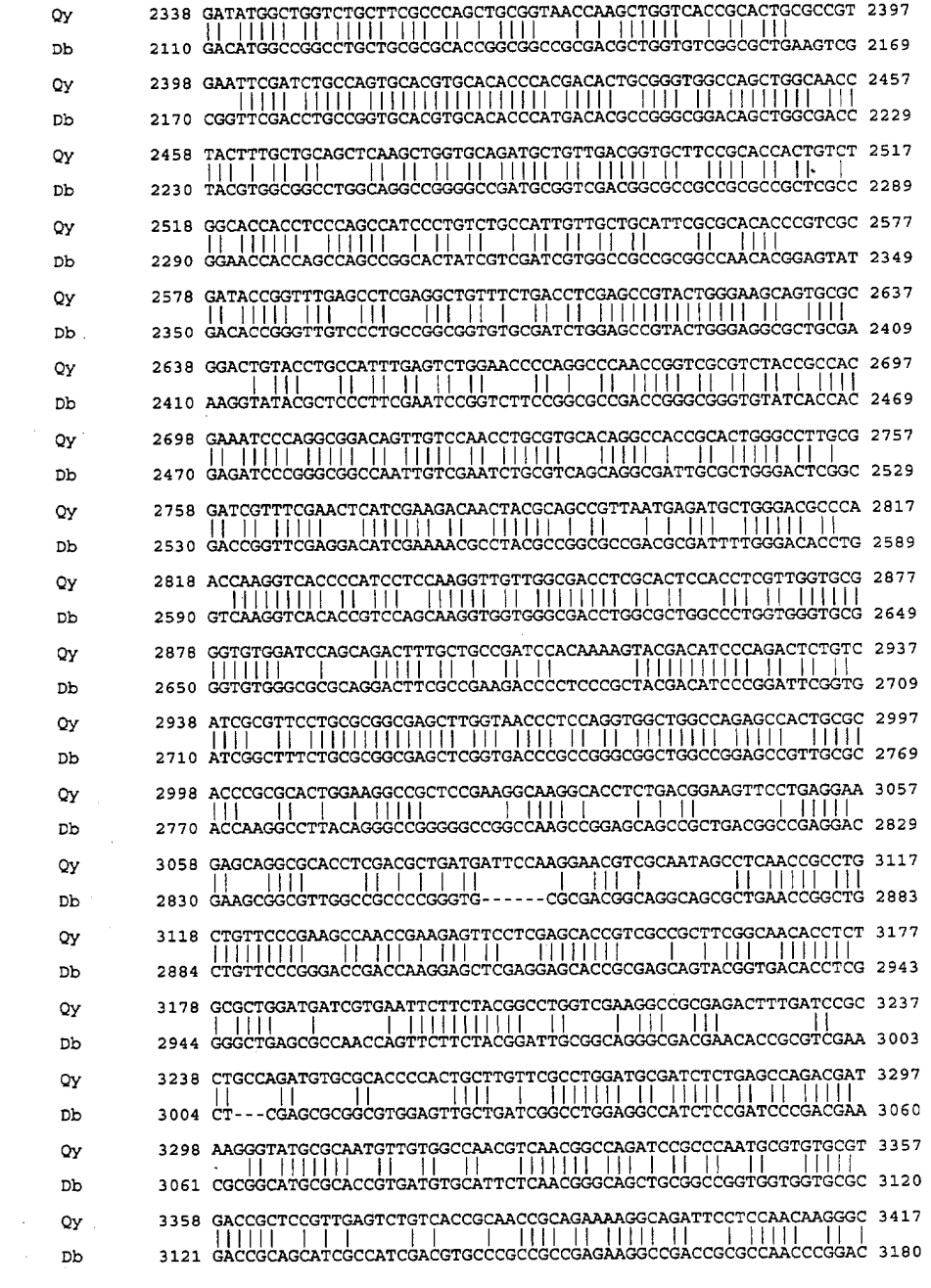
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Db 2170 CGGTTCGACCTGCCGGTGCACGTGCACACCCATGACACGCCGGGCGGACAGCTGGCGACC 2229
Qy 2458 TACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCT 2517
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Db 2290 GGAACCACCAGCCAGCCGGCACTATCGTCGATCGTGGCCGCCGCGGCCAACACGGAGTAT 2349
Qy 2578 GATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGC 2637
Db 2350 GACACCGGGTTGTCCCTGCCGGCGGTGTGCGATCTGGAGCCGTACTGGGAGGCGCTGCGA 2409
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Db 2410 AAGGTATACGCTCCCTTCGAATCCGGTCTTCCGGCGCCGACCGGGCGGGTGTATCACCAC 2469
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Qy       3478 AAGGCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCT 3537
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Qy       3598 GACTTGATCGTCGT 3611
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RESULT 14
ACA40756
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DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #22413.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU36886.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 28626; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3384 BP; 574 A; 1061 C; 1148 G; 601 T; 0 U; 0 Other;

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  Matches 2099;  Conservative    0;  Mismatches 1276;  Indels    9;  Gaps    3;

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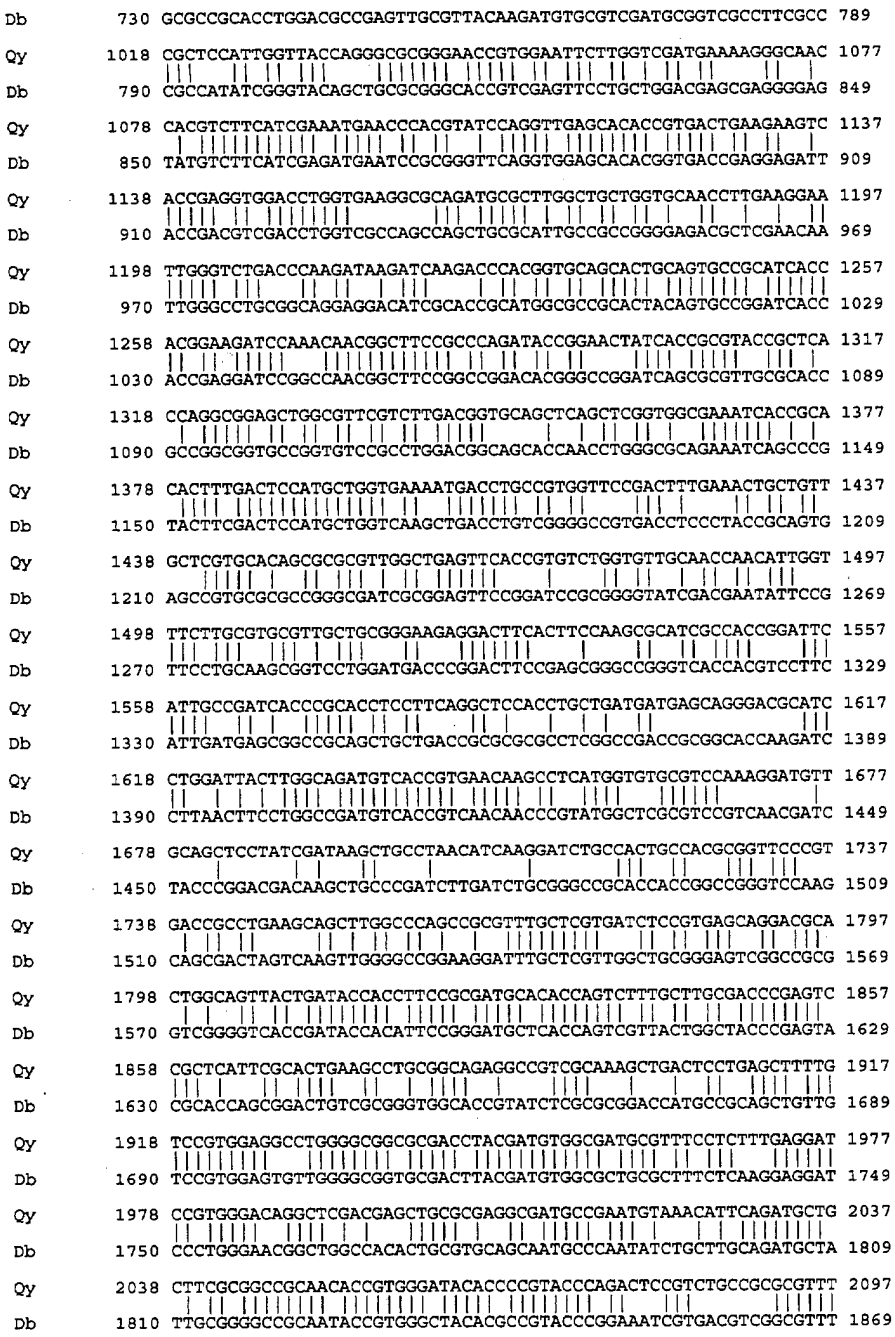
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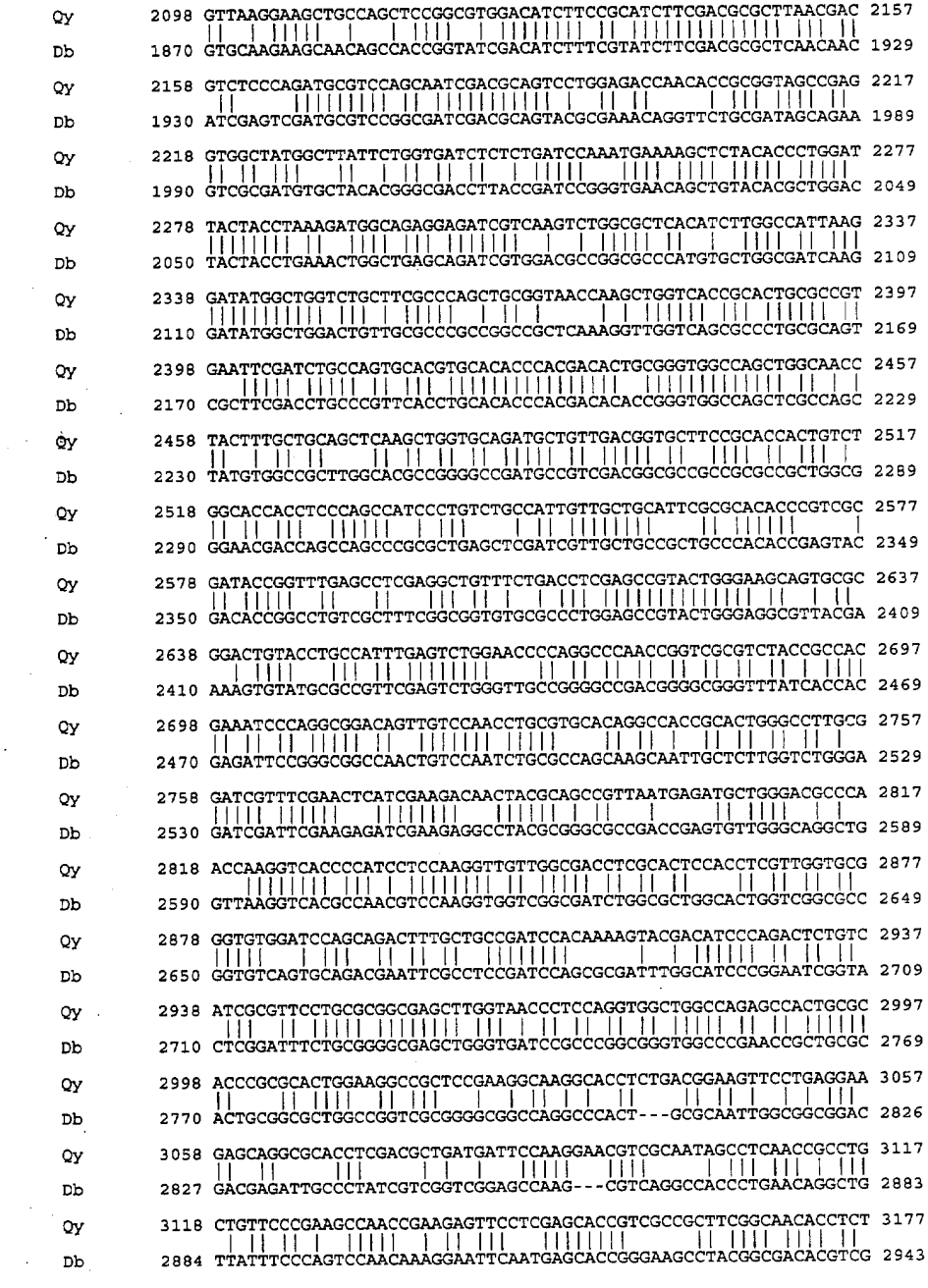
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Qy 2158 GTCTCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAG 2217
Db 1930 ATCGAGTCGATGCGTCCGGCGATCGACGCAGTACGCGAAACAGGTTCTGCGATAGCAGAA 1989
Qy 2218 GTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGAT 2277
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Db 2110 GATATGGCTGGACTGTTGCGCCCGCCGGCCGCTCAAAGGTTGGTCAGCGCCCTGCGCAGT 2169
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Qy 2518 GGCACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGC 2577
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Qy 2578 GATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGC 2637
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RESULT 15
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Query Match 35.7%; Score 1294.4; DB 4; Length 110000;
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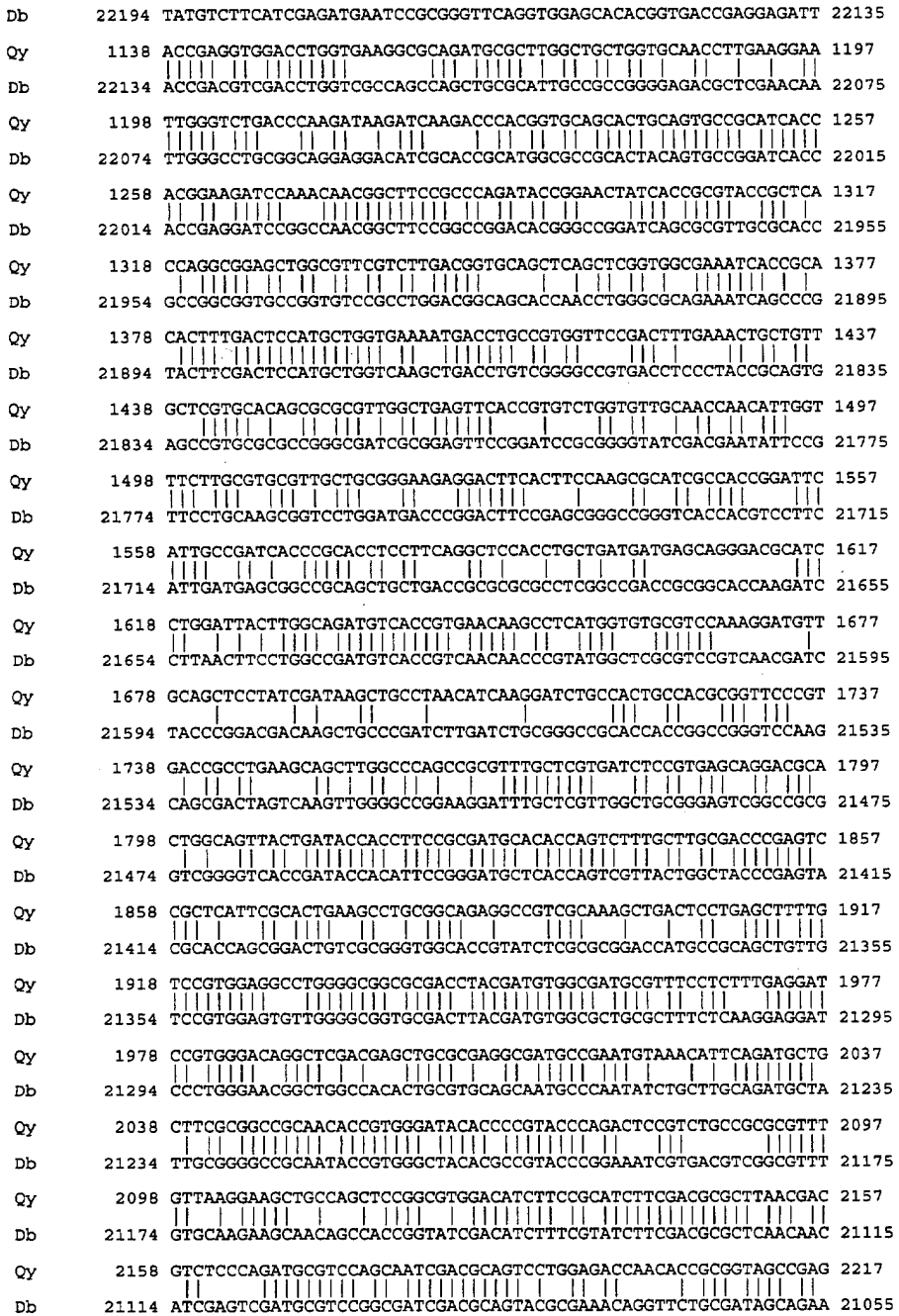

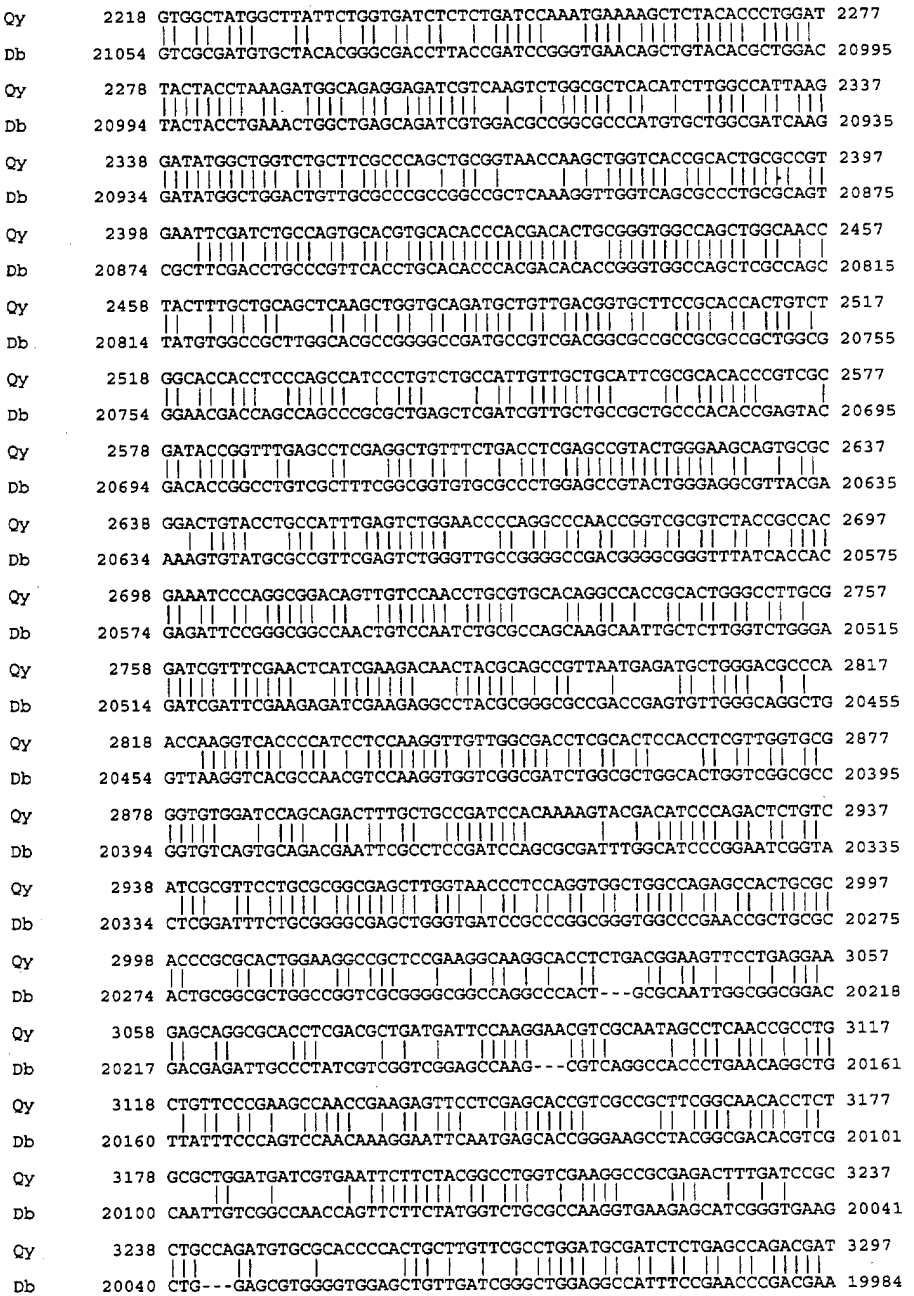

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Job time : 1318 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 17:20:33 ; Search time 237 Seconds
(without alignments)
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Title: US-10-045-072-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	3621	100.0	3621	4	US-09-677-575-1	Sequence 1, Appli
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ALIGNMENTS

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; Sequence 1, Application US/09220081
; Patent No. 6171833
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/220,081
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
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; NAME/KEY: CDS
; LOCATION: (199)..(3621)
US-09-220-081-1

Query Match 100.0%; Score 3621; DB 3; Length 3621;
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Qy       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
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Db       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240

Qy       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300

Qy       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3361 CGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCAT 3420

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RESULT 2
US-09-677-575-1
; Sequence 1, Application US/09677575
; Patent No. 6403351
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/677,575
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/220,081
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(3621)
US-09-677-575-1

Query Match 100.0%; Score 3621; DB 4; Length 3621;
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Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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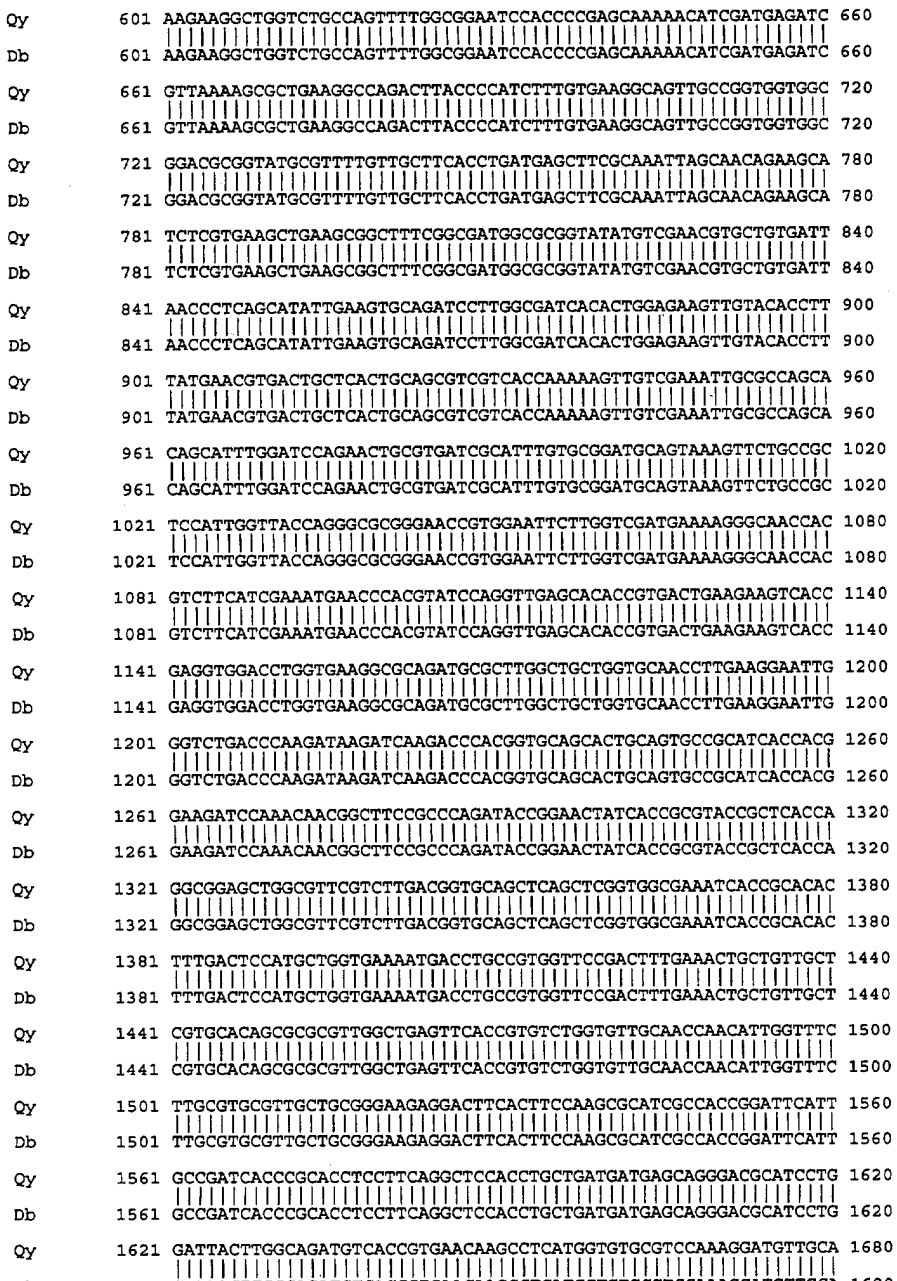
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; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match            35.7%;  Score 1294.4;  DB 3;  Length 4403765;
  Best Local Similarity  62.0%;  Pred. No. 0;
  Matches 2099;  Conservative    0;  Mismatches 1276;  Indels    9;  Gaps    3;

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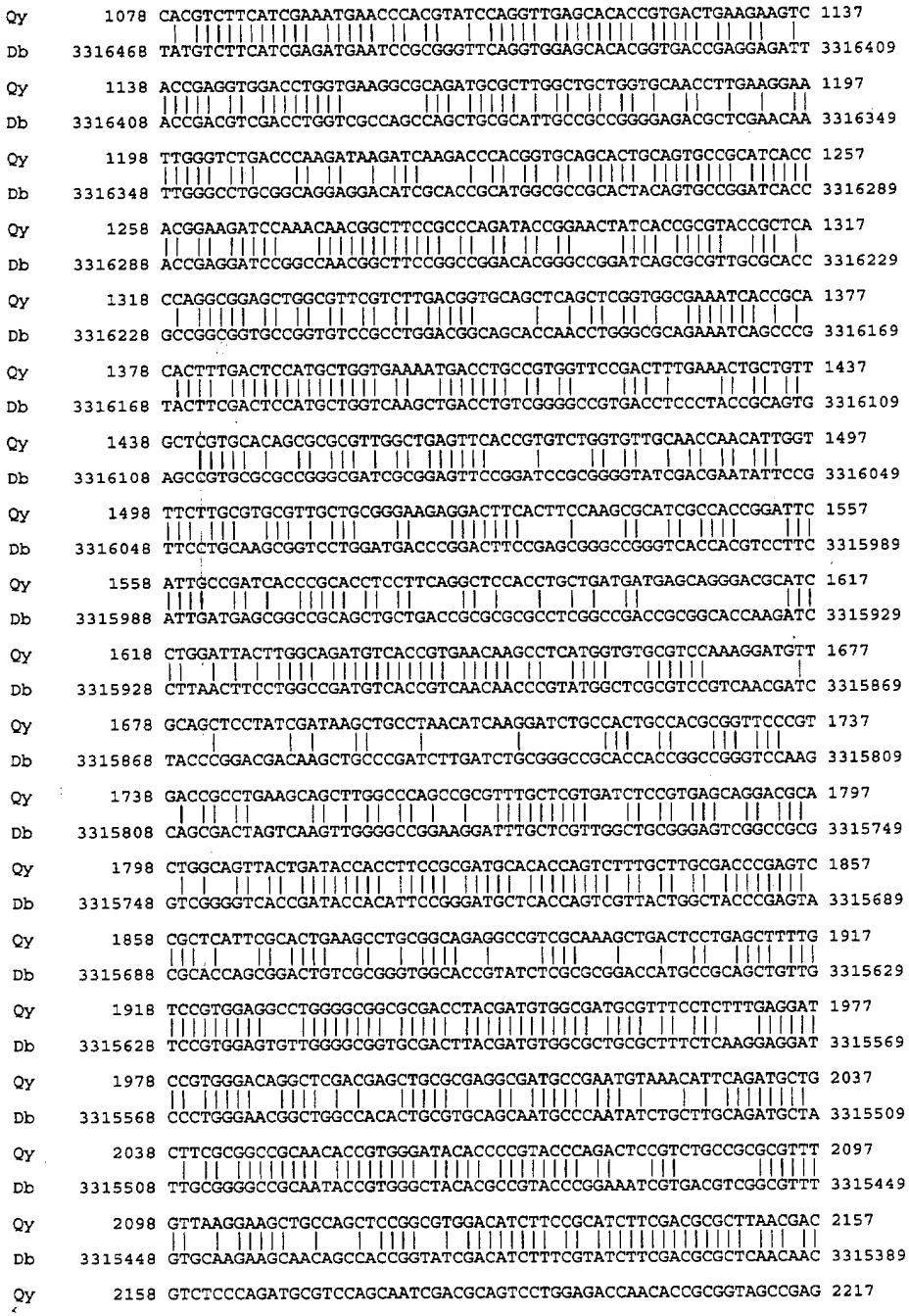
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Qy 1618 CTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTT 1677
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Qy 1678 GCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGT 1737
Db 3315868 TACCCGGACGACAAGCTGCCCGATCTTGATCTGCGGGCCGCACCACCGGCCGGGTCCAAG 3315809
Qy 1738 GACCGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCA 1797
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RESULT 4
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             35.7%;  Score 1294.4;  DB 3;  Length 4411529;
  Best Local Similarity   62.0%;  Pred. No. 0;
  Matches 2099;  Conservative    0;  Mismatches 1276;  Indels    9;  Gaps    3;

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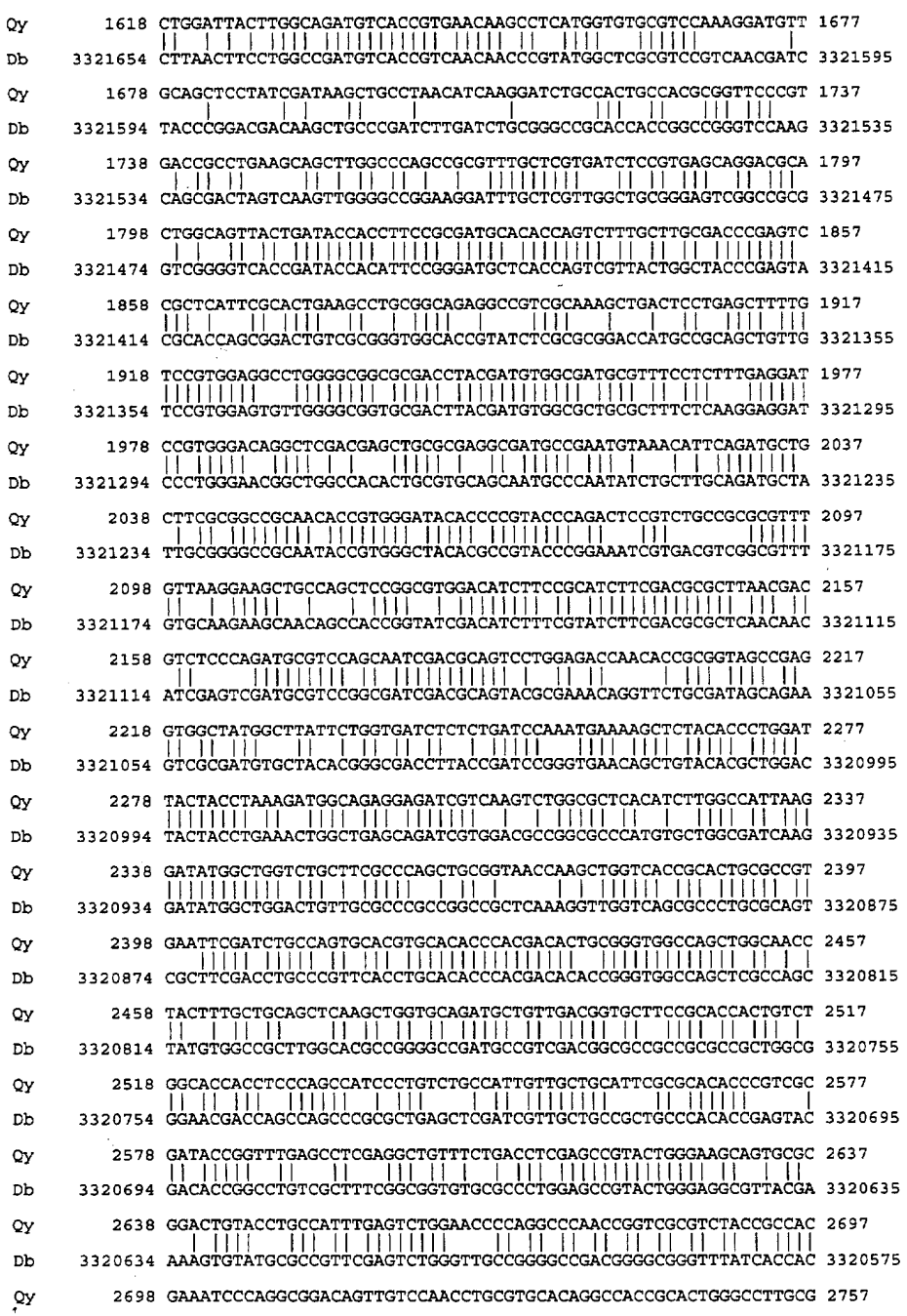
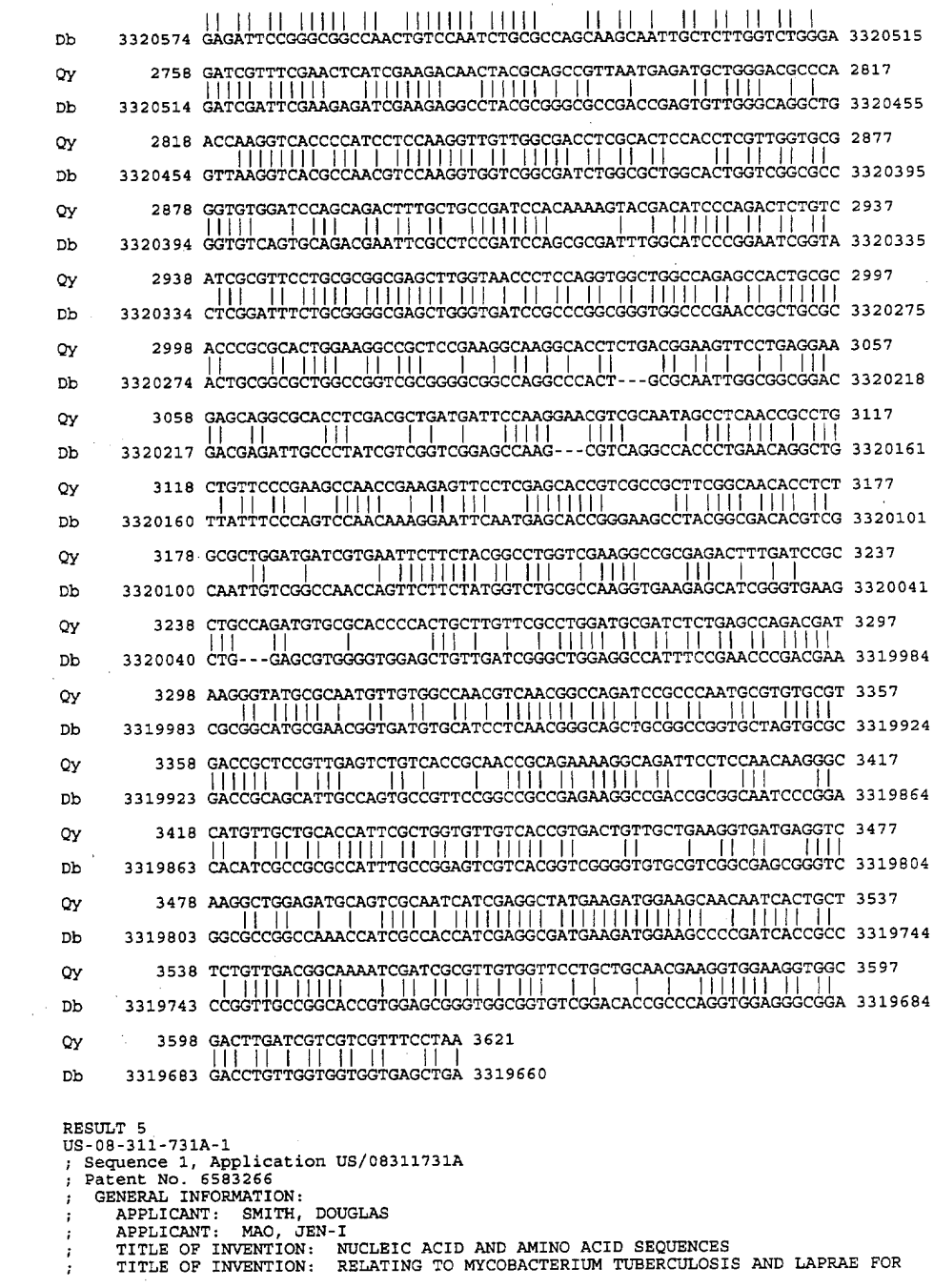
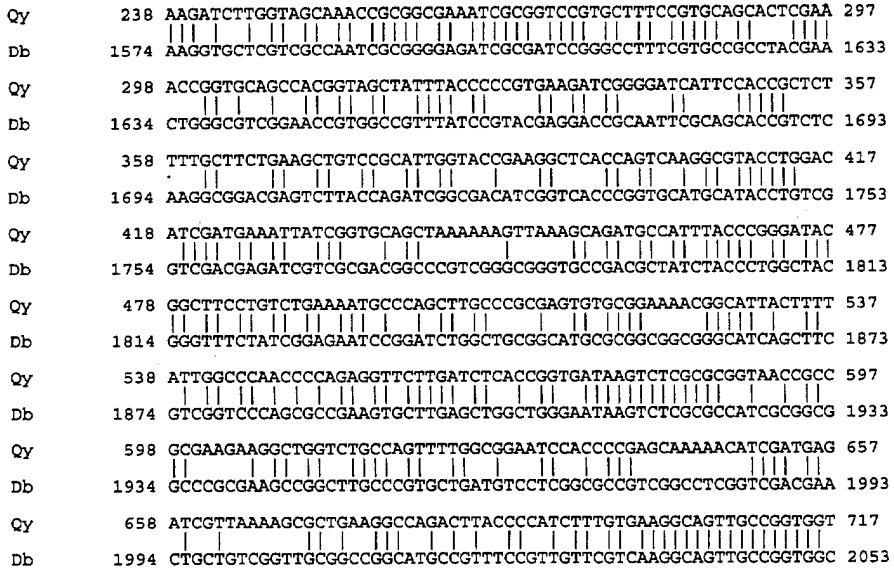


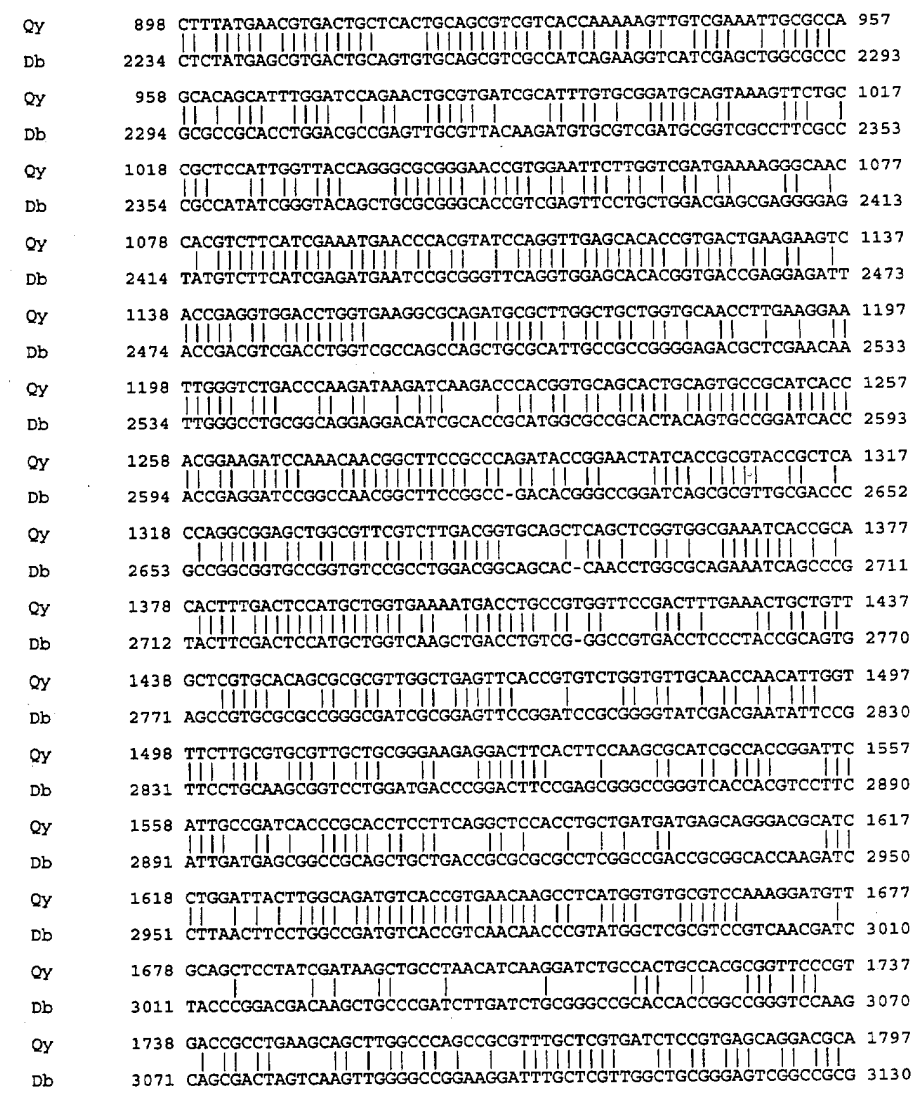


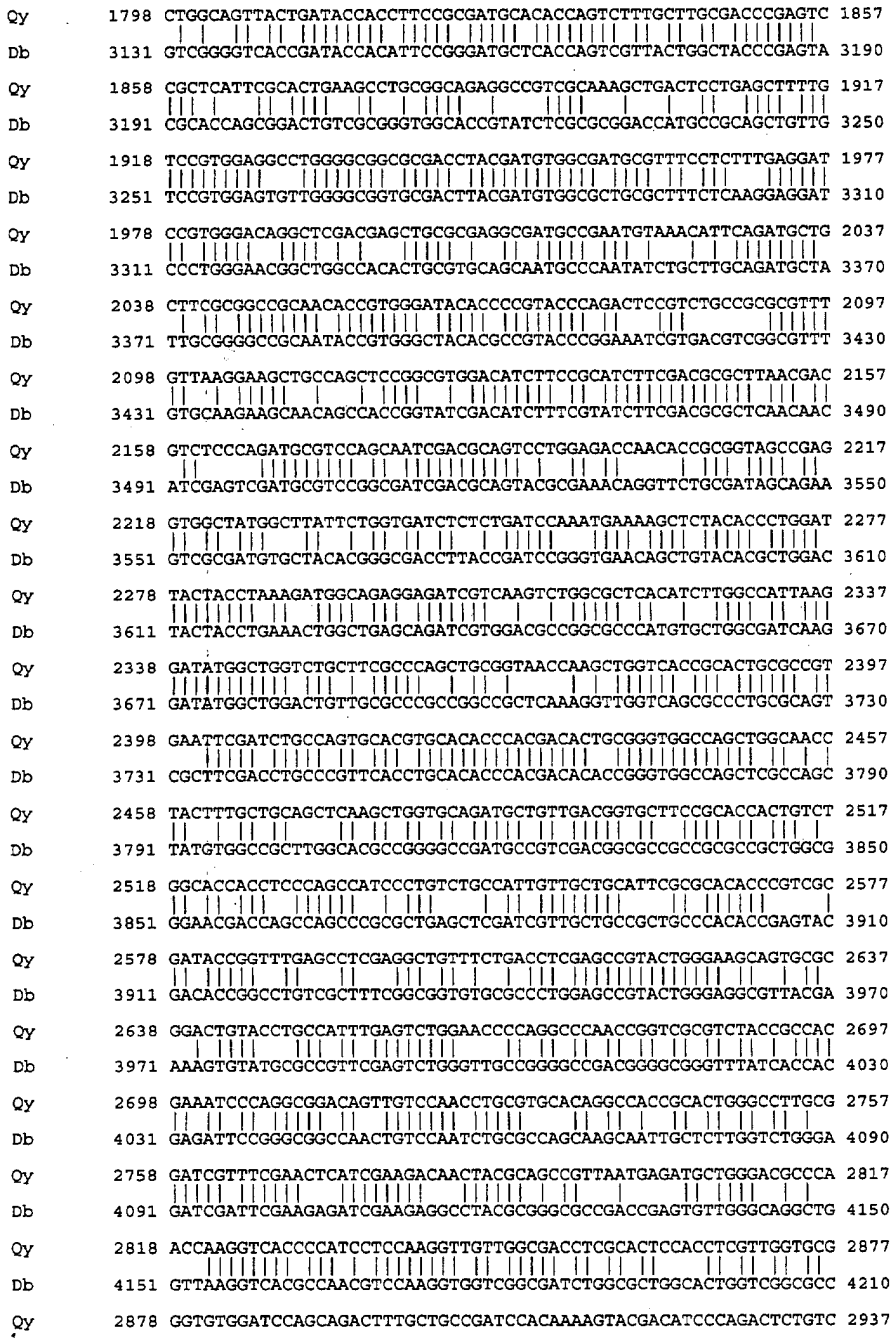
RESULT 5
US-08-311-731A-1
; Sequence 1, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR

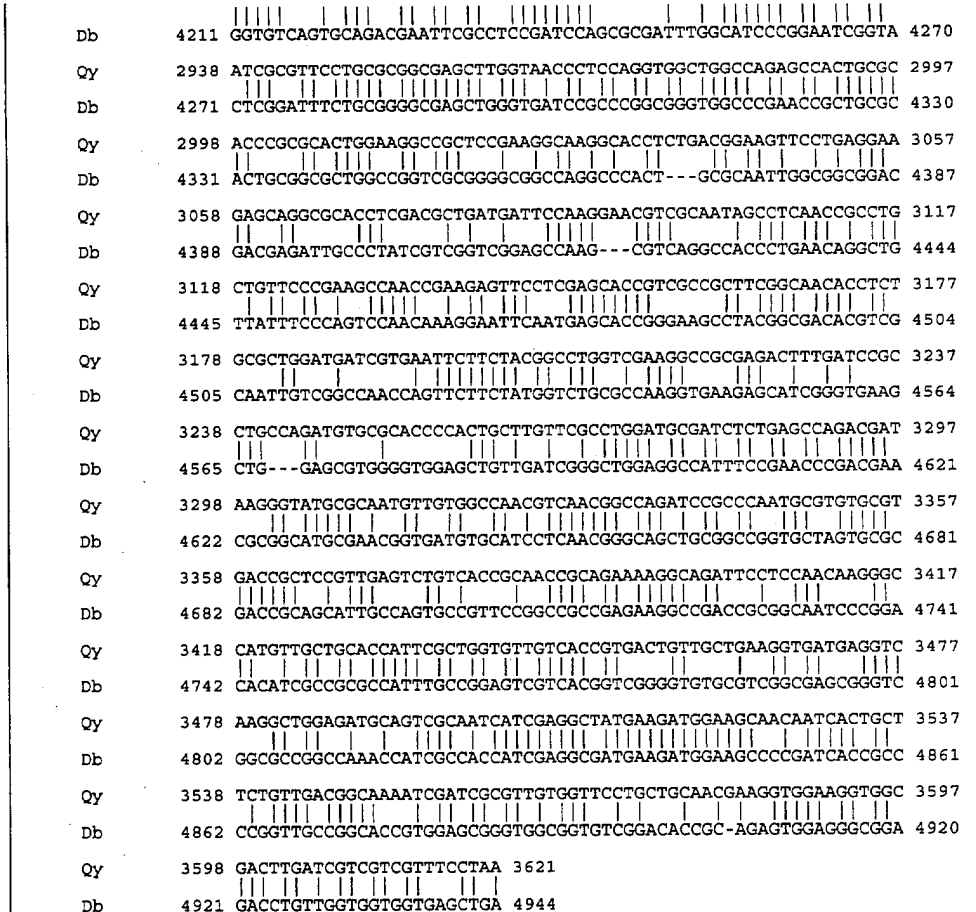
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM TUBERCULOSIS
US-08-311-731A-1

Query Match 34.5%; Score 1249.6; DB 4; Length 32155;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 1274; Indels 13; Gaps 7;



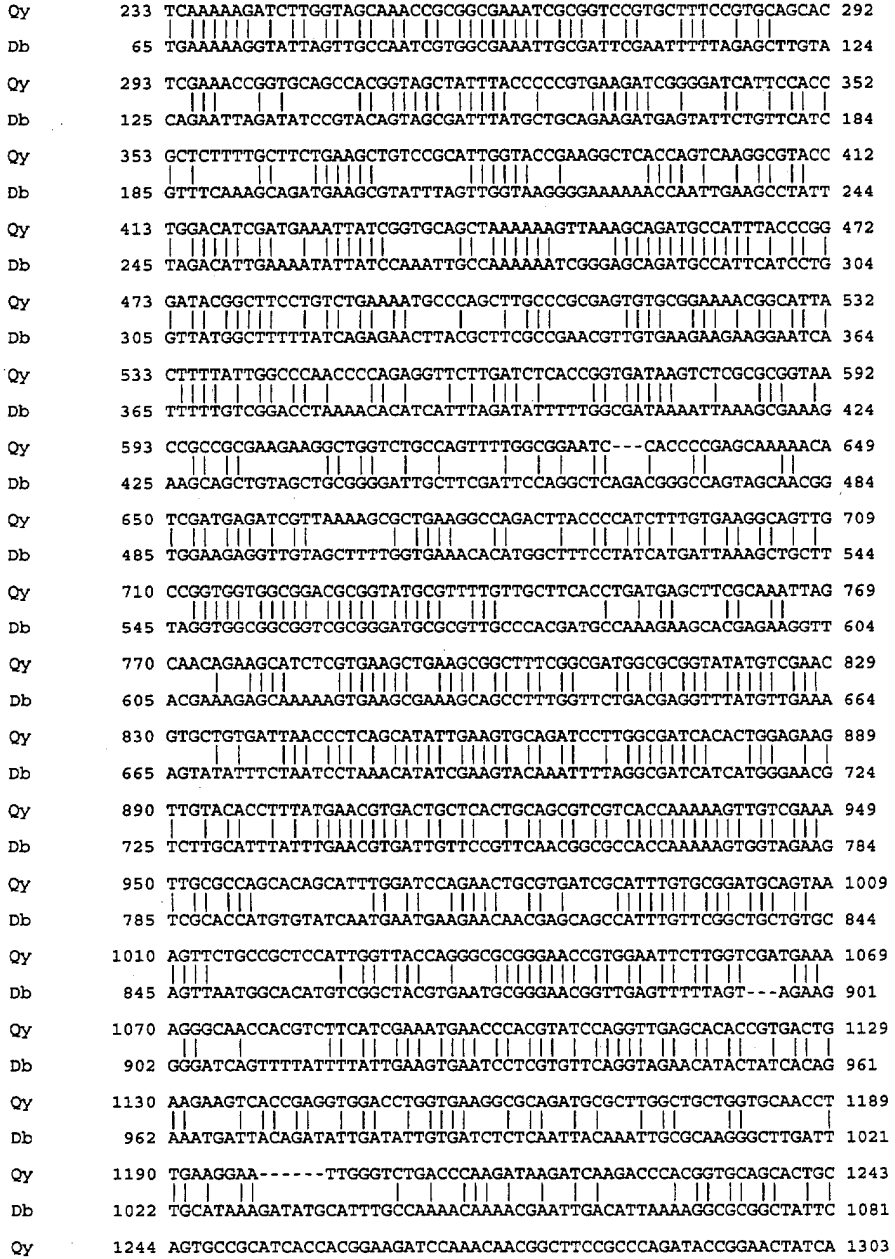


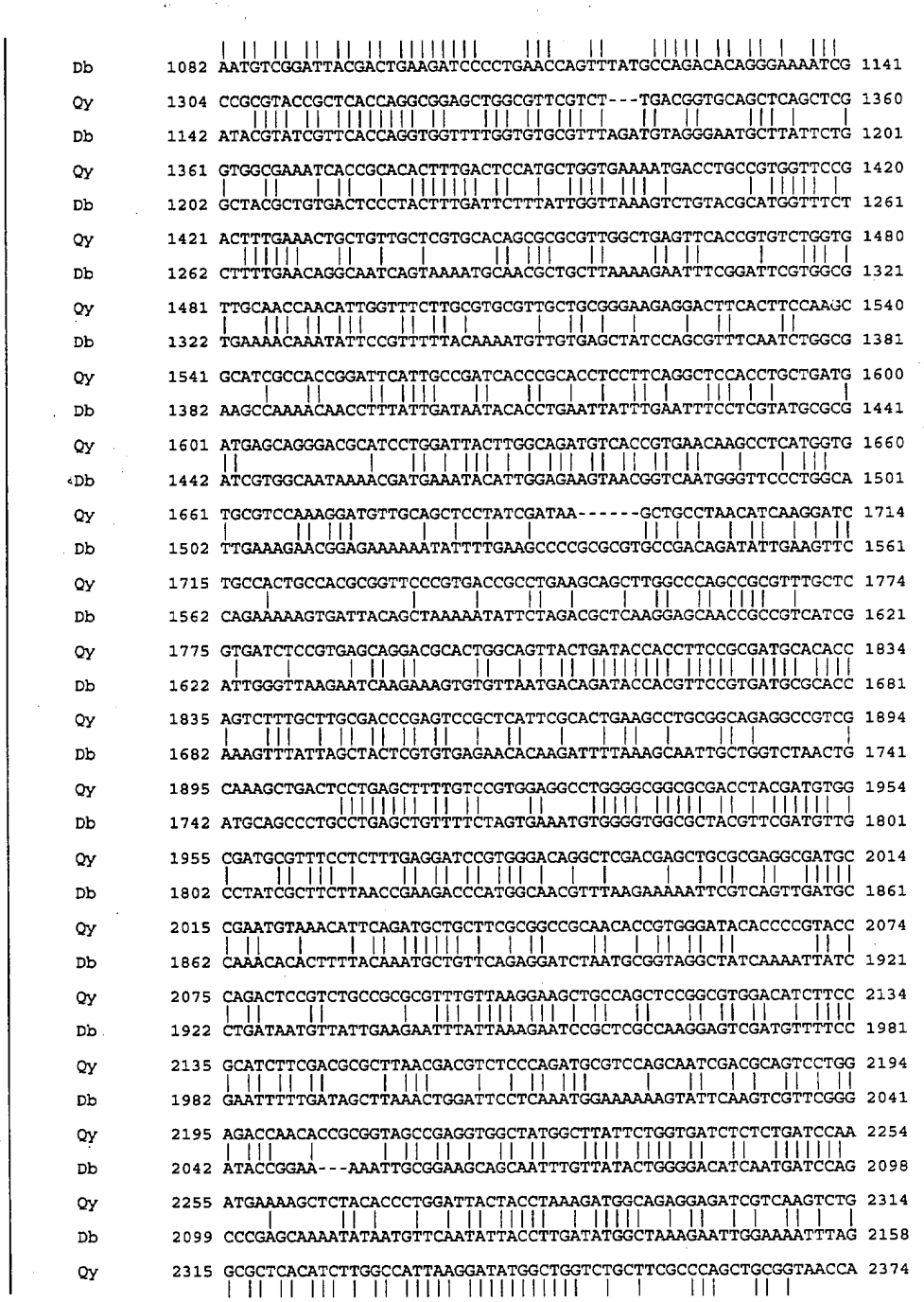


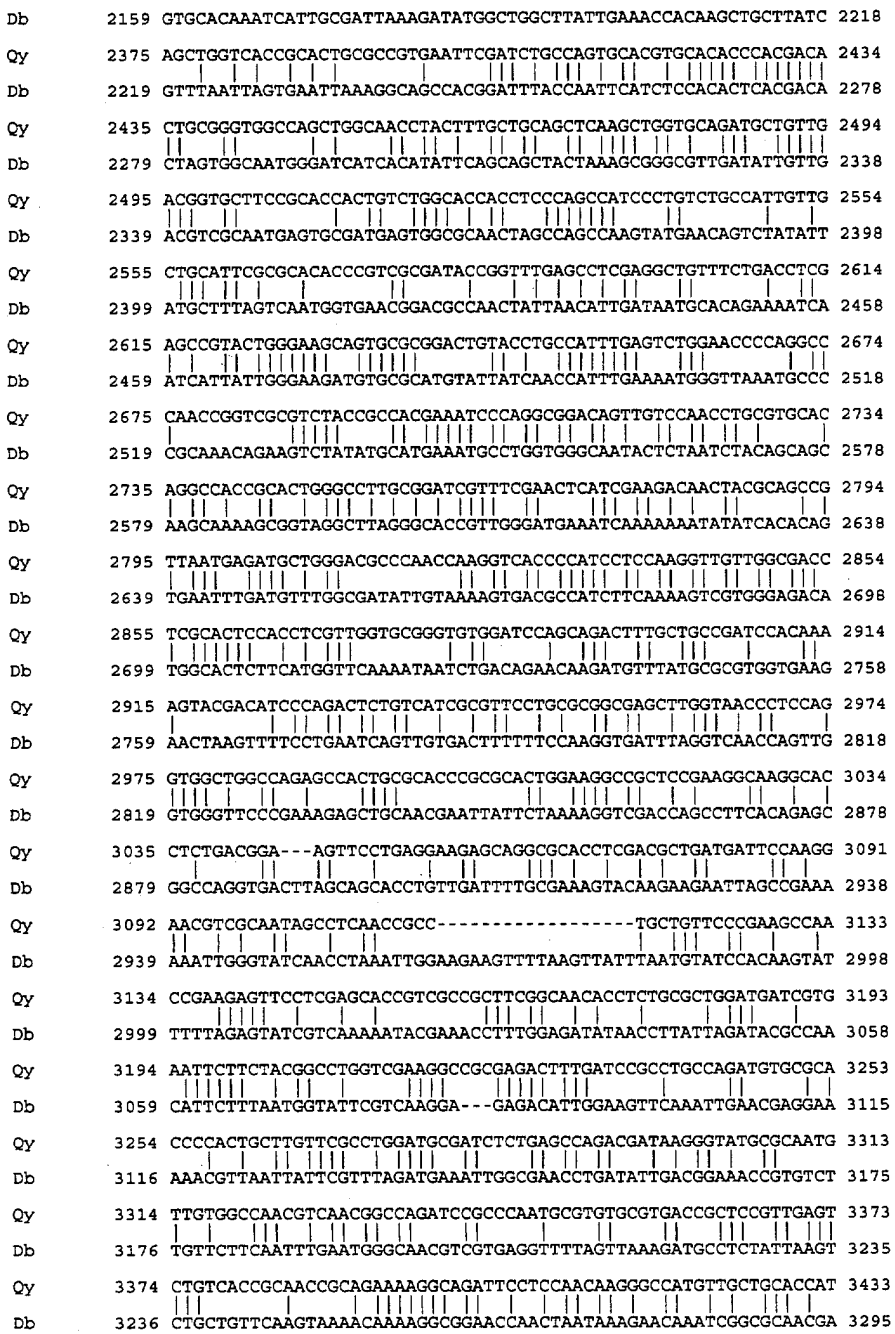


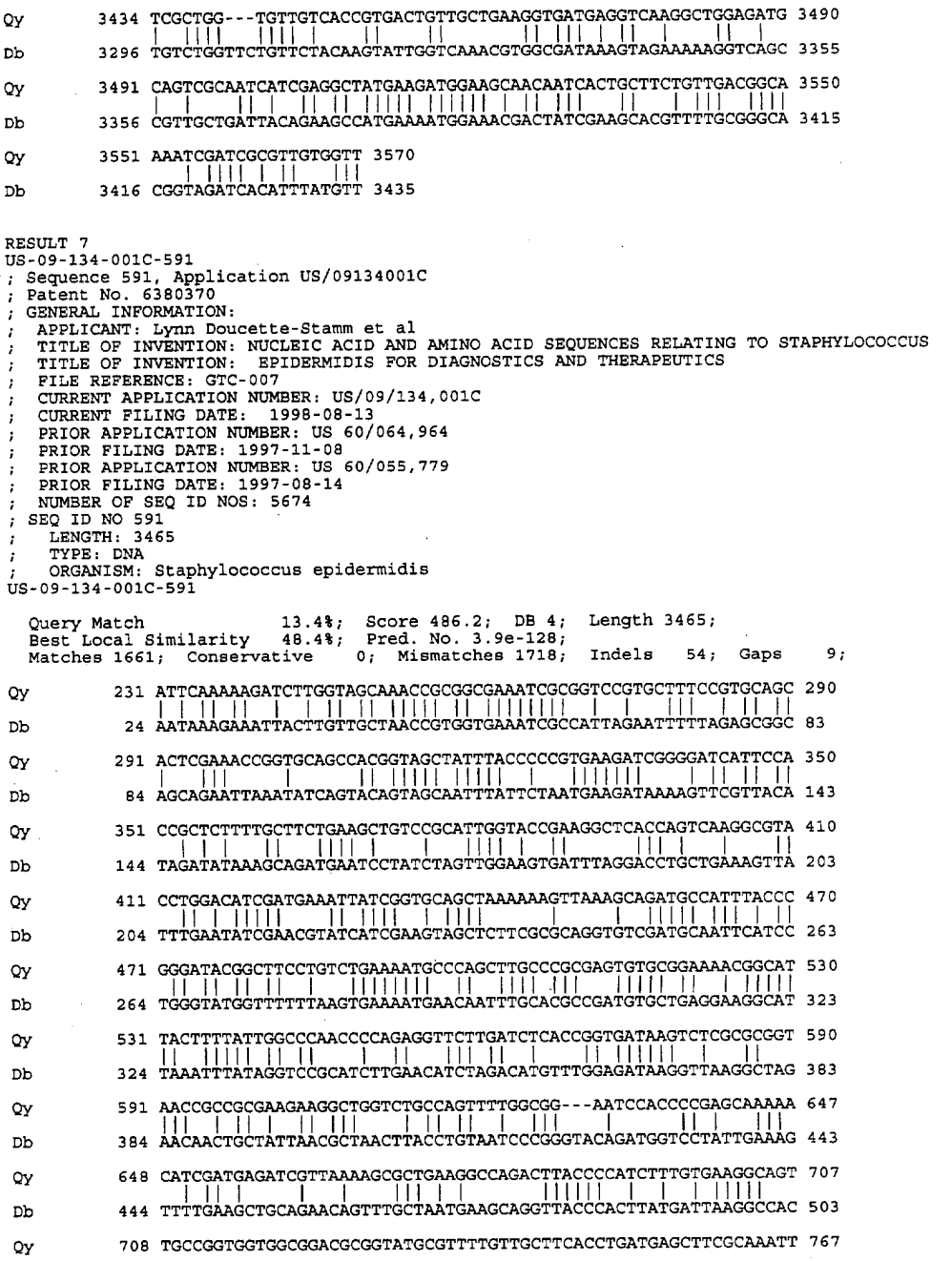
RESULT 6
US-09-134-000C-2302
; Sequence 2302, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2302
; LENGTH: 3492
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2302

Query Match 14.1%; Score 509.2; DB 4; Length 3492;
Best Local Similarity 49.1%; Pred. No. 1.1e-134;
Matches 1661; Conservative 0; Mismatches 1668; Indels 51; Gaps 10;



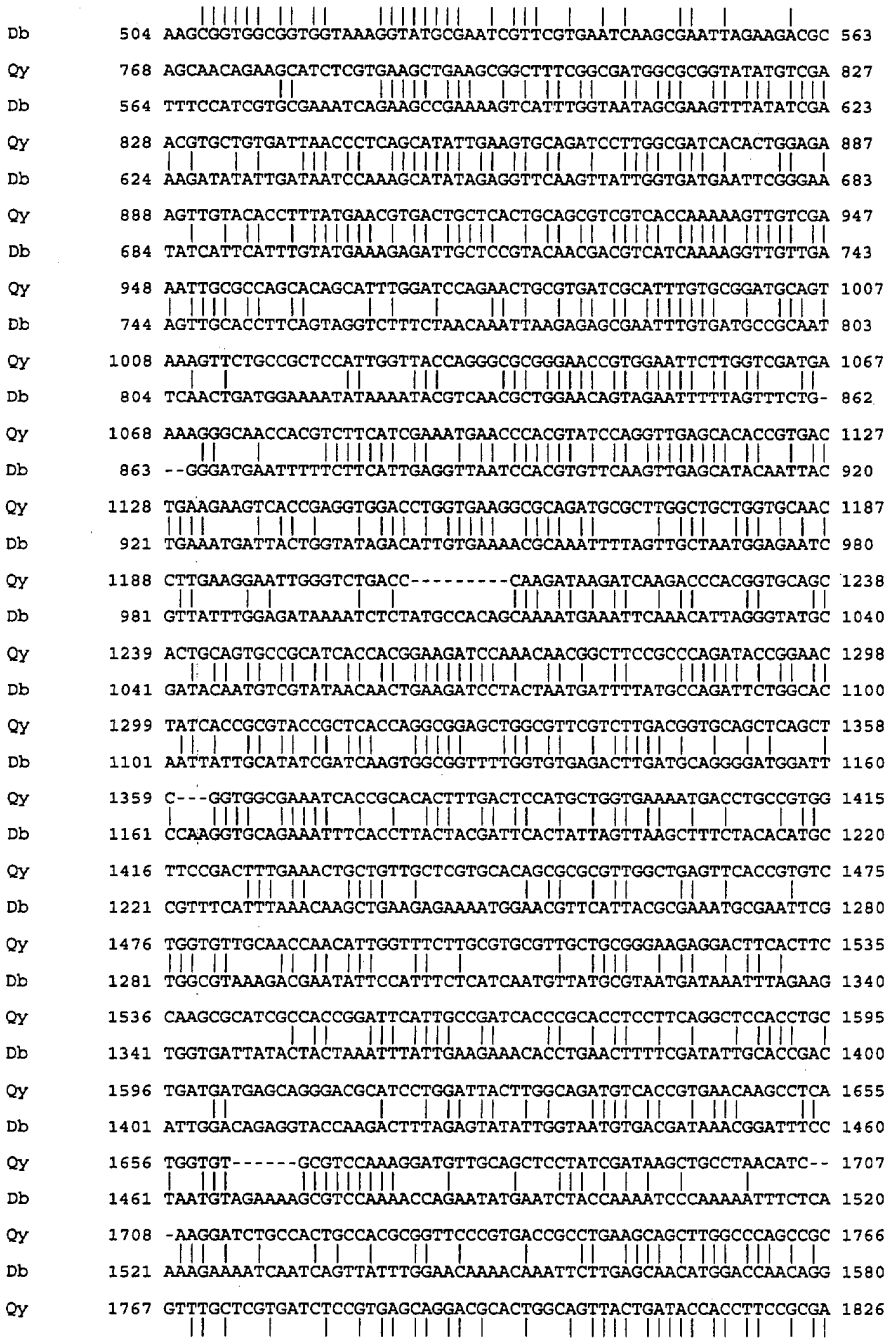






RESULT 7
US-09-134-001C-591
; Sequence 591, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 591
; LENGTH: 3465
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-591

Query Match 13.4%; Score 486.2; DB 4; Length 3465;
Best Local Similarity 48.4%; Pred. No. 3.9e-128;
Matches 1661; Conservative 0; Mismatches 1718; Indels 54; Gaps 9;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Db 624 AAGATATATTGATAATCCAAAGCATATAGAGGTTCAAGTTATTGGTGATGAATTCGGGAA 683
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Qy 1239 ACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAAC 1298
Db 1041 GATACAATGTCGTATAACAACTGAAGATCCTACTAATGATTTTATGCCAGATTCTGGCAC 1100
Qy 1299 TATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCT 1358
Db 1101 AATTATTGCATATCGATCAAGTGGCGGTTTTGGTGTGAGACTTGATGCAGGGGATGGATT 1160
Qy 1359 C---GGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGG 1415
Db 1161 CCAAGGTGCAGAAATTTCACCTTACTACGATTCACTATTAGTTAAGCTTTCTACACATGC 1220
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Qy 1476 TGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTC 1535
Db 1281 TGGCGTAAAGACGAATATTCCATTTCTCATCAATGTTATGCGTAATGATAAATTTAGAAG 1340
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Db 1341 TGGTGATTATACTACTAAATTTATTGAAGAAACACCTGAACTTTTCGATATTGCACCGAC 1400
Qy 1596 TGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCA 1655
Db 1401 ATTGGACAGAGGTACCAAGACTTTAGAGTATATTGGTAATGTGACGATAAACGGATTTCC 1460
Qy 1656 TGGTGT------GCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATC-- 1707
Db 1461 TAATGTAGAAAAGCGTCCAAAACCAGAATATGAATCTACCAAAATCCCAAAAATTTCTCA 1520
Qy 1708 -AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGC 1766
Db 1521 AAAGAAAATCAATCAGTTATTTGGAACAAAACAAATTCTTGAGCAACATGGACCAACAGG 1580
Qy 1767 GTTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGA 1826
Db 1581 TGTTACAAATTGGGTTAGAGAACAAGAAGATGTTTTAATTACCGATACTACATTTAGAGA 1640
Qy 1827 TGCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGA 1886
Db 1641 TGCACACCAATCTTTACTTGCAACACGTGTAAGAACAAAAGATATGATGAACATTGCATC 1700
Qy 1887 GGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTA 1946
Db 1701 TAAAACTGCTGAAGTTTTTAAAGATAGTTTTTCATTAGAAATGTGGGGTGGTGCAACATT 1760
Qy 1947 CGATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGA 2006
Db 1761 TGATGTCGCCTATAATTTCTTGAAAGAGAATCCATGGGAACGTTTAGAAAGATTGCGCAA 1820
Qy 2007 GGCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACAC 2066
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Db 1941 TGTTTTCCGTATATTCGACTCATTGAACTGGGTTGATCAAATGAAAGTAGCGAATGAAGC 2000
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Qy 2307 CAAGTCTGGCGCTCACATCTTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGC 2366
Db 2121 AAGAGAAGGATTCCATATATTAGCAATTAAAGATATGGCTGGTTTATTGAAACCGAAAGC 2180
Qy 2367 GGTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACAC 2426
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Qy 2427 CCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGCAGA 2486
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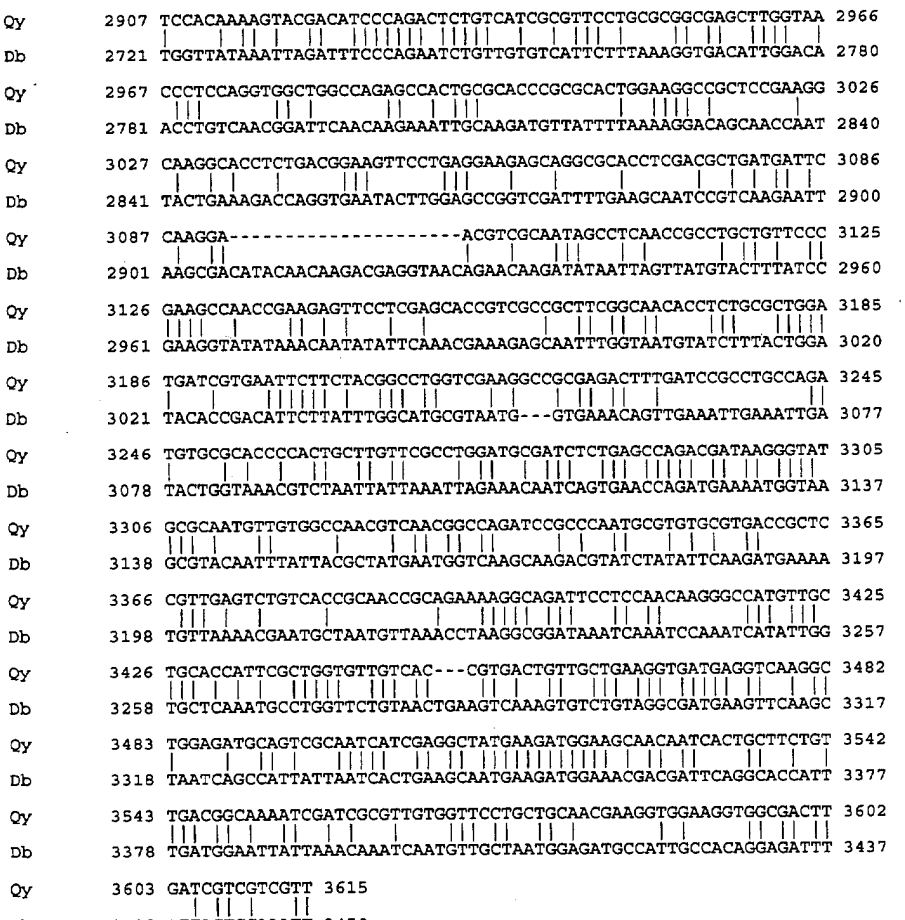

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RESULT 8
US-08-956-171E-324/c
; Sequence 324, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;       APPLICANT: Charles Kunsch
;                  Gil H. Choi
;                  Patrick S. Dillon
;                  Craig A. Rosen
;                  Steven C. Barash
;                  Michael R. Fannon
;       TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;       NUMBER OF SEQUENCES: 5256
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Human Genome Sciences, Inc.
;            STREET: 9410 Key West Avenue
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;            COMPUTER: HP Vectra 486/33
;            OPERATING SYSTEM: MSDOS version 6.2
;            SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/956,171E
;            FILING DATE: 20-Oct-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/009,861
;            FILING DATE: January 5, 1996
;            APPLICATION NUMBER: 08/781,986
;            FILING DATE: January 3, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mark J. Hyman
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB248P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (240) 314-1224
;            TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 324:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 5030 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 324:
US-08-956-171E-324

  Query Match             13.3%;  Score 479.8;  DB 4;  Length 5030;
  Best Local Similarity   48.3%;  Pred. No. 3.3e-126;
  Matches 1657;  Conservative    0;  Mismatches 1722;  Indels   54;  Gaps    9;
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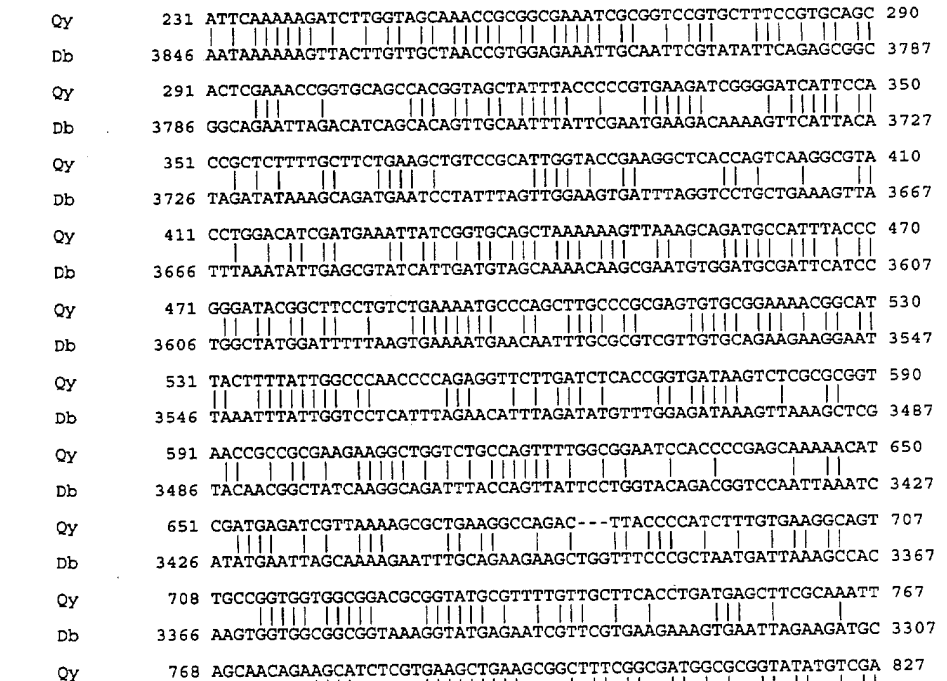

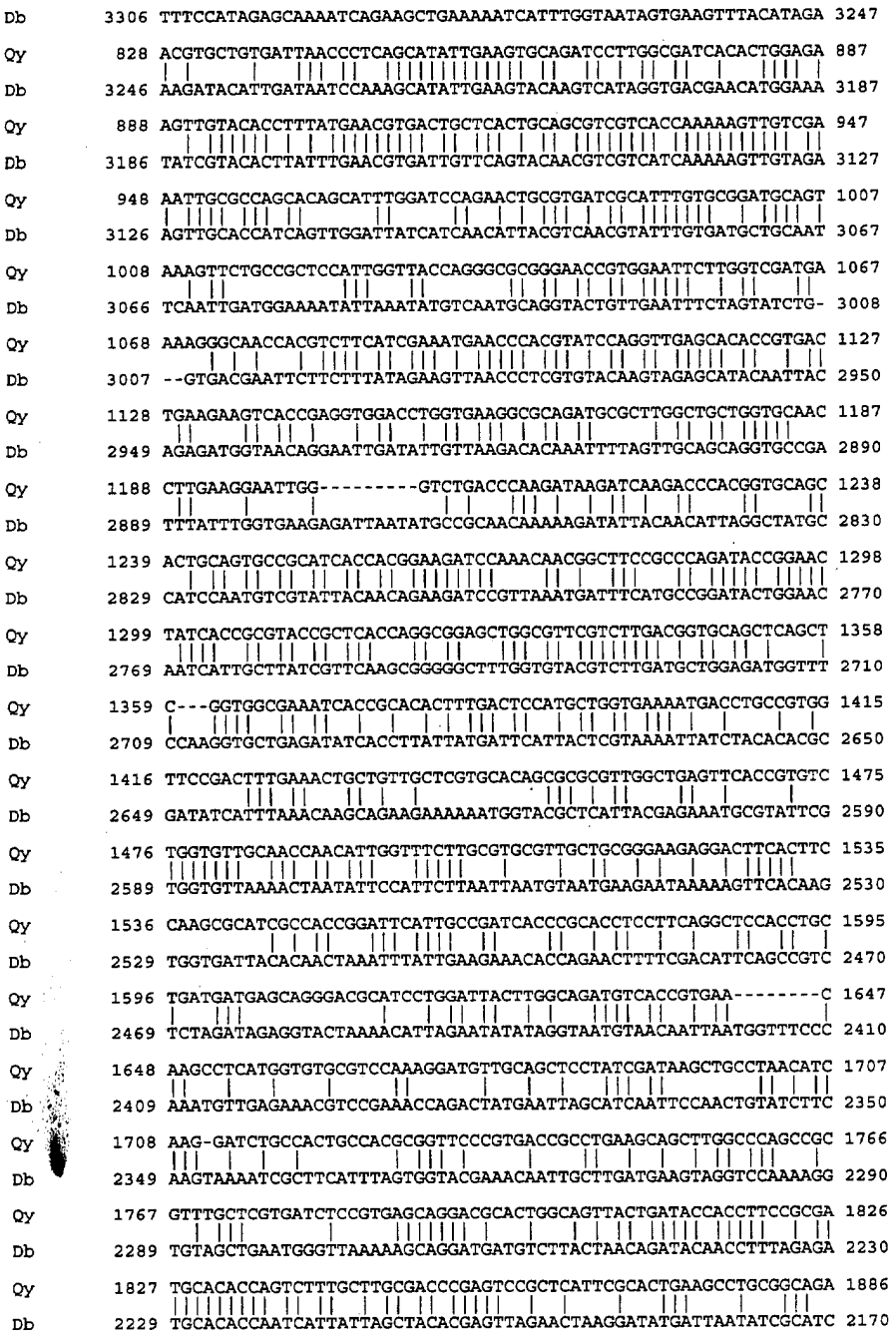

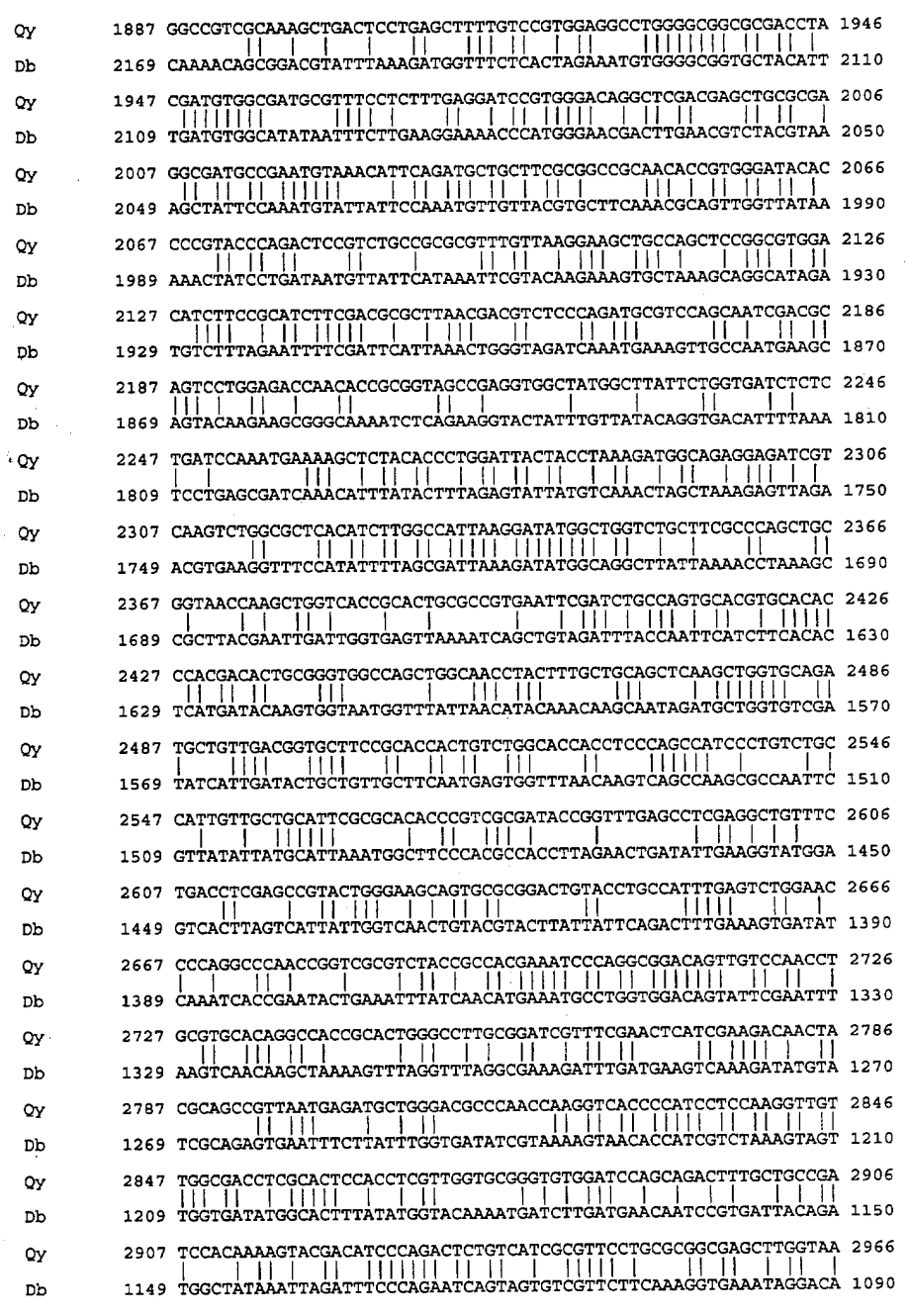

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Qy       3027 CAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTC 3086
Db       1029 AACAGCTCGTCCAGGTGAATATCTAGAGCCAGTTGATTTTGAAAAAGTCCGTGAGTTGCT 970

Qy       3087 CAAGGAACGTCGCAATAGCC--------------------TCAACCGCCTGCTGTTCCC 3125
Db        969 TGAAGAAGAGCAACAAGGTCCTGTTACGGAGCAAGATATTATTAGTTATGTACTATATCC 910

Qy       3126 GAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGA 3185
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Qy       3186 TGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTGCCAGA 3245
Db        849 TACGCCTACATTCTTCTTTGGAATGCGTAATG---GTGAAACAGTAGAAATCGAAATCGA 793

Qy       3246 TGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTAT 3305
Db        792 TAAAGGTAAACGATTAATTATTAAACTAGAAACGATTAGTGAACCAGATGAAAATGGTAA 733

Qy       3306 GCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTC 3365
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Qy       3366 CGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGC 3425
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Qy       3426 TGCACCATTCGCTGGTGTTGTCAC---CGTGACTGTTGCTGAAGGTGATGAGGTCAAGGC 3482
Db        612 TGCTCAAATGCCAGGTTCAGTAACTGAAGTCAAGGTTAGTGTAGGTGAAACTGTGAAAGC 553

Qy       3483 TGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGT 3542
Db        552 TAATCAGCCGTTGCTAATTACTGAAGCTATGAAAATGGAAACAACAATTCAAGCACCATT 493

Qy       3543 TGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTT 3602
Db        492 TGACGGTGTGATTAAACAAGTAACTGTAAATAATGGTGACACAATAGCGACAGGCGATTT 433

Qy       3603 GATCGTCGTCGTT 3615
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RESULT 9
US-09-107-532A-1156
; Sequence 1156, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;    INFORMATION FOR SEQ ID NO: 1156:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2922 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...2922
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1156:
US-09-107-532A-1156

  Query Match             13.2%;  Score 476.2;  DB 4;  Length 2922;
  Best Local Similarity   49.9%;  Pred. No. 2.5e-125;
  Matches 1425;  Conservative    0;  Mismatches 1408;  Indels   24;  Gaps    8;
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Qy        259 GGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCT 318
Db         61 GGTGAAATCGCTGTACGTGTATTTCGTGCTTGTACAGAATTAGGAATTAAAACTGTTGGA 120

Qy        319 ATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGC 378
Db        121 ATCTATGCAGAAAAAAATGAATATTCCGTACACCGTTTCAAAGCGGATGAAGCATATTTA 180

Qy        379 ATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCA 438
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Qy        676 GGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGT 735
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Qy        736 TTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAA 795
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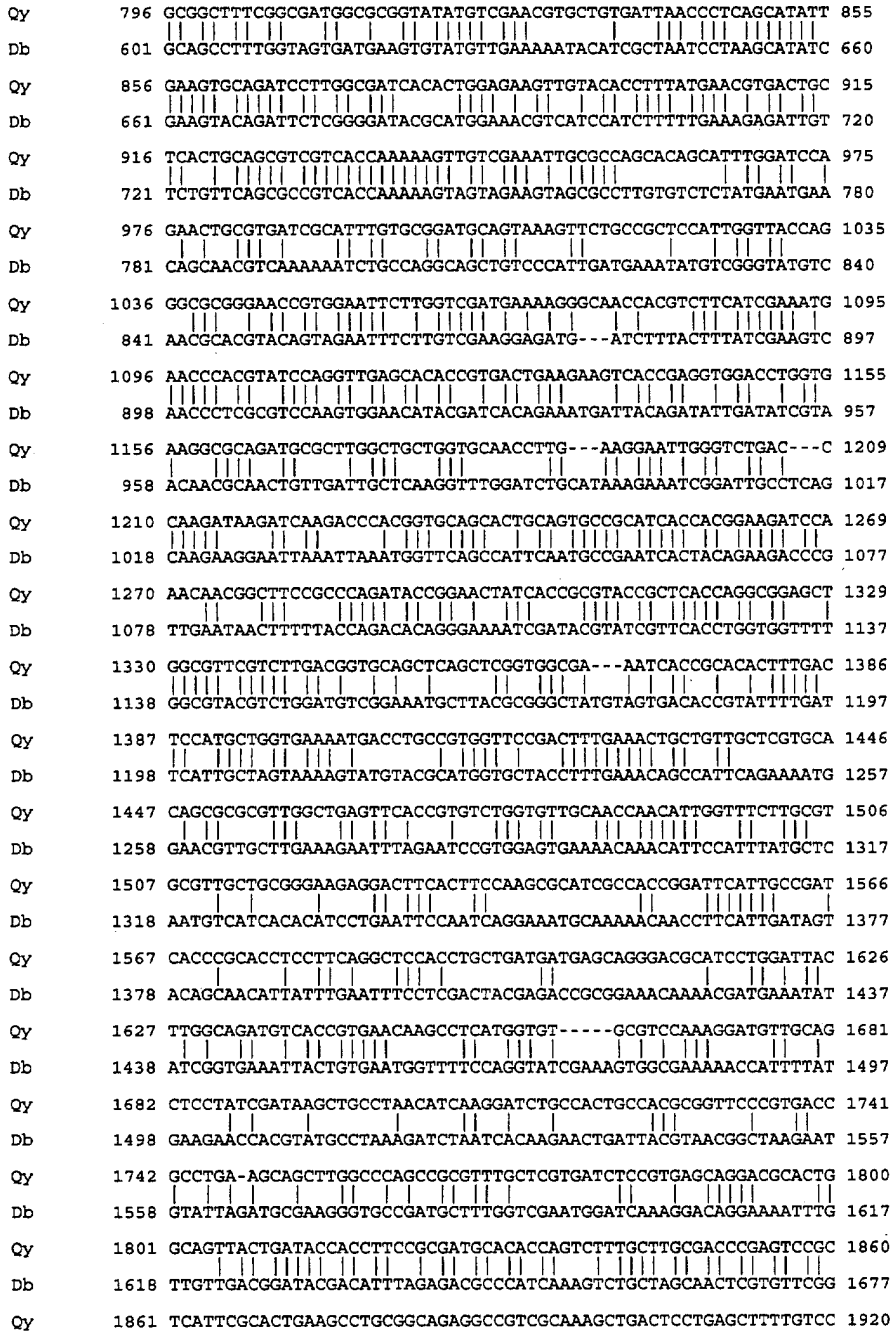

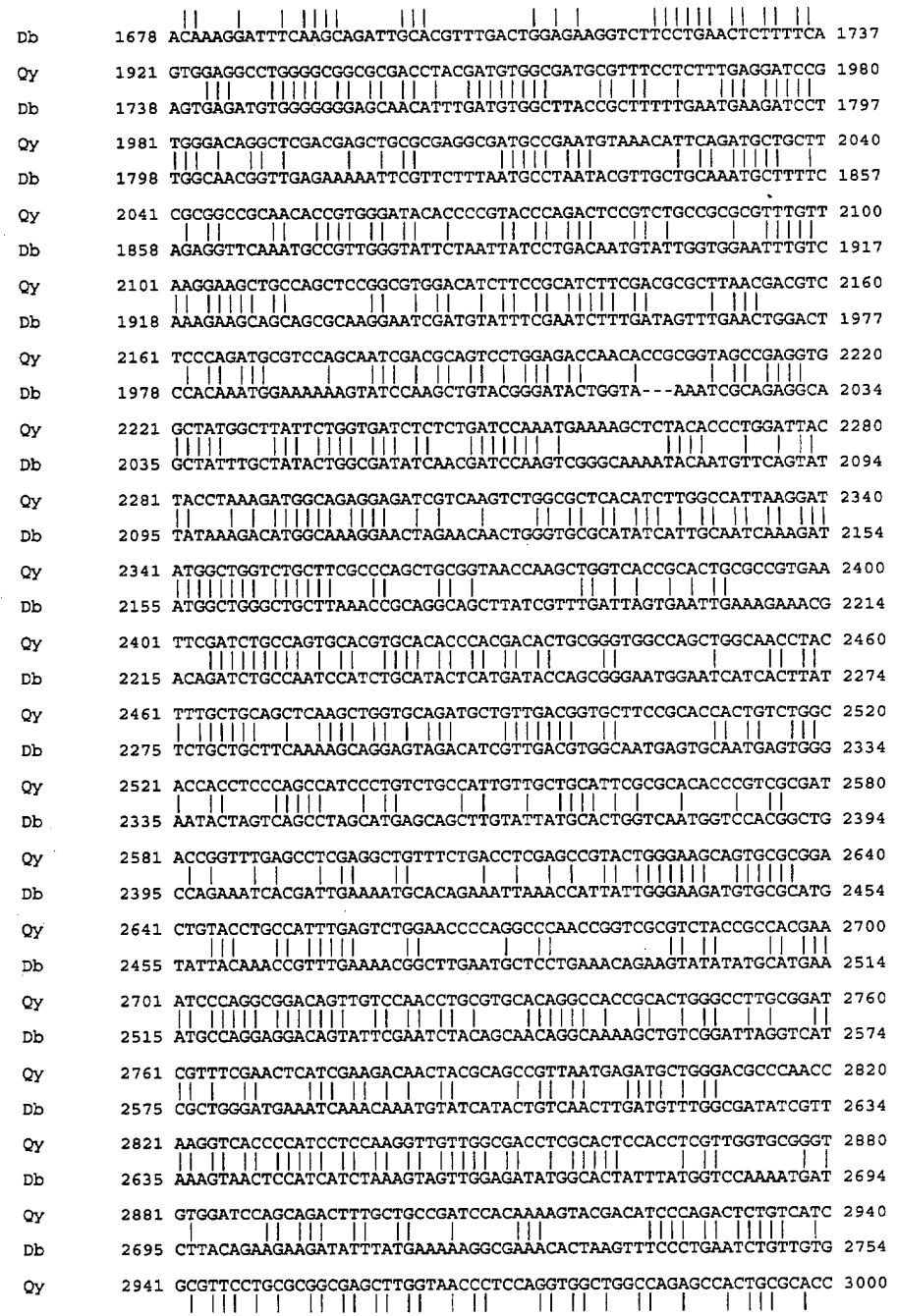

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Db     2815 ATTATTCTTAAAGGCAGACCTGCATTGAATGAACGTC 2851
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RESULT 10
US-09-543-681A-1699
; Sequence 1699, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1699
;   LENGTH: 1362
;   TYPE: DNA
;   ORGANISM: Proteus mirabilis
US-09-543-681A-1699

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  Best Local Similarity   55.4%;  Pred. No. 4.4e-79;
  Matches  721;  Conservative    0;  Mismatches  556;  Indels   24;  Gaps    5;

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Qy      356 CTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGG 415
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Qy      476 ACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTT 535
Db      257 ATGGCTTCCTGTCTGAAAATGCCGATTTTGCCGAACAAGTTGAACGCTCAGGCTTTATTT 316

Qy      536 TTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCG 595
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Qy      596 CCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATC------CACCCCGAGCAAAAACA 649
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Qy      770 CAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAAC 829
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Qy      830 GTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAG 889
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Qy     1190 TGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCC 1249
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Qy     1430 CTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCA 1489
Db     1202 TTGCGATTTCTCGTATGAAAAATGCGTTGGCAGAACTTATTATTGACGGCATTAAAACCA 1261

Qy     1490 ACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTC 1530
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RESULT 11
US-07-956-700B-5
; Sequence 5, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
;   APPLICANT: Robert Haselkorn and Piotr Gornicki
;   TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
;   TITLE OF INVENTION: Carboxylase
;   NUMBER OF SEQUENCES: 116
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: 321 No. 5539092th Clark Street
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60610
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy Disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII-DOS
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/956,700B
;   FILING DATE: 19921002
;   CLASSIFICATION: 800
;   ATTORNEY/AGENT INFORMATION:

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;      NAME:  Thomas E. No. 5539092thrup
;      REGISTRATION NUMBER:  33,268
;      REFERENCE/DOCKET NUMBER:  ARCD:058
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-312-744-0090
;      TELEFAX:  1-312-755-4489
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1362 base pairs
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Oligonucleotide
US-07-956-700B-5

  Query Match             8.6%;  Score 313;  DB 1;  Length 1362;
  Best Local Similarity   53.9%;  Pred. No. 5.7e-79;
  Matches  718;  Conservative    0;  Mismatches  600;  Indels   15;  Gaps    3;

Qy       232 TTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCA 291
Db         7 TTCAACAAGATCCTGATCGCCAATCGCGGCGAAATCGCCCTGCGCATTCTCCGCACTTGT 66

Qy       292 CTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCAC 351
Db        67 CAAGAACTCGGGATCGGCACGATCGCCGTTCACTCCACTGTGGATCGCAACGCGCTCCAT 126

Qy       352 CGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTAC 411
Db       127 GTGCAGTTAGCGGACGAAGCGGTCTGTATTGG---CGAAGCGGCCAGCAGCAAAAGCTAT 183

Qy       412 CTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCG 471
Db       184 CTCAATATCCCCAACATCATTGCGGCGGCCCTGACCCCTAATGCCAGCGCCATTCACCCC 243

Qy       472 GGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATT 531
Db       244 GGCTATGGCTTCTTGGCGGAGAATGCCCGCTTTGCAGAAATCTGCGCCGATCACCATCTC 303

Qy       532 ACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGC---G 588
Db       304 ACCTTTATTGGCCCCAGCCCCGATTCGATTCGAGCCATGGGCGATAAATCCACCGCTAAG 363

Qy       589 GTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAAC 648
Db       364 GAAACAATGCAGCGGGTCGGCGTTCCGACGATTCCGGGCAGTGACGGTCTGCTGACGGAT 423

Qy       649 ATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTT 708
Db       424 GTTGATTCGGCTGCCAAAGTTGCTGCCGAGATCGGCTATCCCGTCATGATCAAAGCGACG 483

Qy       709 GCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTA 768
Db       484 GCGGGGGGCGGTGGTCGCGGTATGCGGCTGGTGCGTGACCCTGCAGATCTGGAAAAACTG 543

Qy       769 GCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAA 828
Db       544 TTCCTTGCTGCCCAAGGAGAAGCCGAGGCAGCTTTTGGGAATCCAGGACTGTATCTCGAA 603

Qy       829 CGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAA 888
Db       604 AAATTTATCGATCGCCCACGCCACGTTGAATTTCAGATCTTGGCCGATGCCTACGGCAAT 663

Qy       889 GTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAA 948
Db       664 GTAGTGCATCTAGGCGAGCGCGATTGCTCCATTCAACGTCGTCACCAAAAGCTGCTCGAA 723

Qy       949 ATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTA 1008
Db       724 GAAGCCCCCAGTCCGGCGCTATCGGCAGACCTGCGGCAGAAAATGGGCGATGCCGCCGTC 783

Qy      1009 AAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAA 1068
Db       784 AAAGTCGCTCAAGCGATCGGCTACATCGGTGCCGGCACCGTGGAGTTTCTGGTCGATGCG 843

Qy      1069 AAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACT 1128
Db       844 ACCGGCAACTTCTACTTCATGGAGATGAATACCCGCATCCAAGTCGAGCATCCAGTCACA 903

Qy      1129 GAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACC 1188
Db       904 GAAATGATTACGGGACTGGACTTGATTGCGGAGCAGATTCGGATTGCCCAAGGCG----- 958

Qy      1189 TTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGC 1248
Db       959 ----AAGCGCTGCGCTTCCGGCAAGCCGATATTCAACTGCGCGGCCATGCGATCGAATGC 1014

Qy      1249 CGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCG 1308
Db      1015 CGTATCAATGCGGAAGATCCGGAATACAATTTCCGGCCGAATCCTGGCCGCATTACAGGC 1074

Qy      1309 TACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAA 1368
Db      1075 TATTTACCGCCCGGCGGCCCCGGCGTTCGTGTCGATTCCCATGTTTATACCGACTACGAA 1134

Qy      1369 ATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAA 1428
Db      1135 ATTCCGCCCTATTACGATTCGCTGATTGGCAAATTGATTGTCTGGGGTGCAACACGGGAA 1194

Qy      1429 ACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACC 1488
Db      1195 GAGGCGATCGCGCGGATGCAGCGTGCTCTGCGGGAATGCGCCATCACCGGCTTGCCGACG 1254

Qy      1489 AACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCC 1548
Db      1255 ACCCTTAGTTTCCATCAGCTGATGTTGCAGATGCCTGAGTTCCTGCGCGGGGAACTCTAT 1314

Qy      1549 ACCGGATTCATTG 1561
Db      1315 ACCAACTTTGTTG 1327


RESULT 12
US-08-476-537-5
; Sequence 5, Application US/08476537
; Patent No. 5756290
;  GENERAL INFORMATION:
;    APPLICANT:  Robert Haselkorn and Piotr Gornicki
;    TITLE OF INVENTION:  Cyanobacterial and Plant Acetyl-CoA
;    TITLE OF INVENTION:  Carboxylase
;    NUMBER OF SEQUENCES:  116
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  321 No. 5756290th Clark Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60610
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,537
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/956,700
;      FILING DATE:  10/21/92
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Thomas E. No. 5756290thrup
;      REGISTRATION NUMBER:  33,268
;      REFERENCE/DOCKET NUMBER:  ARCD:058
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-312-744-0090
```

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;      TELEFAX:  1-312-755-4489
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1362 base pairs
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Oligonucleotide
US-08-476-537-5

  Query Match             8.6%;  Score 313;  DB 1;  Length 1362;
  Best Local Similarity   53.9%;  Pred. No. 5.7e-79;
  Matches  718;  Conservative    0;  Mismatches  600;  Indels   15;  Gaps    3;

Qy       232 TTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCA 291
Db         7 TTCAACAAGATCCTGATCGCCAATCGCGGCGAAATCGCCCTGCGCATTCTCCGCACTTGT 66

Qy       292 CTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCAC 351
Db        67 CAAGAACTCGGGATCGGCACGATCGCCGTTCACTCCACTGTGGATCGCAACGCGCTCCAT 126

Qy       352 CGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTAC 411
Db       127 GTGCAGTTAGCGGACGAAGCGGTCTGTATTGG---CGAAGCGGCCAGCAGCAAAAGCTAT 183

Qy       412 CTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCG 471
Db       184 CTCAATATCCCCAACATCATTGCGGCGGCCCTGACCCCTAATGCCAGCGCCATTCACCCC 243

Qy       472 GGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATT 531
Db       244 GGCTATGGCTTCTTGGCGGAGAATGCCCGCTTTGCAGAAATCTGCGCCGATCACCATCTC 303

Qy       532 ACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGC---G 588
Db       304 ACCTTTATTGGCCCCAGCCCCGATTCGATTCGAGCCATGGGCGATAAATCCACCGCTAAG 363

Qy       589 GTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAAC 648
Db       364 GAAACAATGCAGCGGGTCGGCGTTCCGACGATTCCGGGCAGTGACGGTCTGCTGACGGAT 423

Qy       649 ATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTT 708
Db       424 GTTGATTCGGCTGCCAAAGTTGCTGCCGAGATCGGCTATCCCGTCATGATCAAAGCGACG 483

Qy       709 GCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTA 768
Db       484 GCGGGGGGCGGTGGTCGCGGTATGCGGCTGGTGCGTGACCCTGCAGATCTGGAAAAACTG 543

Qy       769 GCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAA 828
Db       544 TTCCTTGCTGCCCAAGGAGAAGCCGAGGCAGCTTTTGGGAATCCAGGACTGTATCTCGAA 603

Qy       829 CGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAA 888
Db       604 AAATTTATCGATCGCCCACGCCACGTTGAATTTCAGATCTTGGCCGATGCCTACGGCAAT 663

Qy       889 GTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAA 948
Db       664 GTAGTGCATCTAGGCGAGCGCGATTGCTCCATTCAACGTCGTCACCAAAAGCTGCTCGAA 723

Qy       949 ATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTA 1008
Db       724 GAAGCCCCCAGTCCGGCGCTATCGGCAGACCTGCGGCAGAAAATGGGCGATGCCGCCGTC 783

Qy      1009 AAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAA 1068
Db       784 AAAGTCGCTCAAGCGATCGGCTACATCGGTGCCGGCACCGTGGAGTTTCTGGTCGATGCG 843

Qy      1069 AAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACT 1128
Db       844 ACCGGCAACTTCTACTTCATGGAGATGAATACCCGCATCCAAGTCGAGCATCCAGTCACA 903

Qy      1129 GAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACC 1188
Db       904 GAAATGATTACGGGACTGGACTTGATTGCGGAGCAGATTCGGATTGCCCAAGGCG----- 958

Qy      1189 TTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGC 1248
Db       959 ----AAGCGCTGCGCTTCCGGCAAGCCGATATTCAACTGCGCGGCCATGCGATCGAATGC 1014

Qy      1249 CGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCG 1308
Db      1015 CGTATCAATGCGGAAGATCCGGAATACAATTTCCGGCCGAATCCTGGCCGCATTACAGGC 1074

Qy      1309 TACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAA 1368
Db      1075 TATTTACCGCCCGGCGGCCCCGGCGTTCGTGTCGATTCCCATGTTTATACCGACTACGAA 1134

Qy      1369 ATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAA 1428
Db      1135 ATTCCGCCCTATTACGATTCGCTGATTGGCAAATTGATTGTCTGGGGTGCAACACGGGAA 1194

Qy      1429 ACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACC 1488
Db      1195 GAGGCGATCGCGCGGATGCAGCGTGCTCTGCGGGAATGCGCCATCACCGGCTTGCCGACG 1254

Qy      1489 AACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCC 1548
Db      1255 ACCCTTAGTTTCCATCAGCTGATGTTGCAGATGCCTGAGTTCCTGCGCGGGGAACTCTAT 1314

Qy      1549 ACCGGATTCATTG 1561
Db      1315 ACCAACTTTGTTG 1327


RESULT 13
US-08-485-607-5
; Sequence 5, Application US/08485607
; Patent No. 5792627
;  GENERAL INFORMATION:
;    APPLICANT:  Robert Haselkorn and Piotr Gornicki
;    TITLE OF INVENTION:  Cyanobacterial and Plant Acetyl-CoA
;    TITLE OF INVENTION:  Carboxylase
;    NUMBER OF SEQUENCES:  116
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  321 No. 5792627th Clark Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60610
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,607
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/956,700
;      FILING DATE:  10/21/92
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Thomas E. No. 5792627thrup
;      REGISTRATION NUMBER:  33,268
;      REFERENCE/DOCKET NUMBER:  ARCD:058
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-312-744-0090
;      TELEFAX:  1-312-755-4489
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1362 base pairs
;      TYPE:  Nucleic acid
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;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Oligonucleotide
US-08-485-607-5

  Query Match             8.6%;  Score 313;  DB 1;  Length 1362;
  Best Local Similarity   53.9%;  Pred. No. 5.7e-79;
  Matches  718;  Conservative    0;  Mismatches  600;  Indels   15;  Gaps    3;

Qy        232 TTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCA 291
Db          7 TTCAACAAGATCCTGATCGCCAATCGCGGCGAAATCGCCCTGCGCATTCTCCGCACTTGT 66

Qy        292 CTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCAC 351
Db         67 CAAGAACTCGGGATCGGCACGATCGCCGTTCACTCCACTGTGGATCGCAACGCGCTCCAT 126

Qy        352 CGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTAC 411
Db        127 GTGCAGTTAGCGGACGAAGCGGTCTGTATTGG---CGAAGCGGCCAGCAGCAAAAGCTAT 183

Qy        412 CTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCG 471
Db        184 CTCAATATCCCCAACATCATTGCGGCGGCCCTGACCCCTAATGCCAGCGCCATTCACCCC 243

Qy        472 GGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATT 531
Db        244 GGCTATGGCTTCTTGGCGGAGAATGCCCGCTTTGCAGAAATCTGCGCCGATCACCATCTC 303

Qy        532 ACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGC---G 588
Db        304 ACCTTTATTGGCCCCAGCCCCGATTCGATTCGAGCCATGGGCGATAAATCCACCGCTAAG 363

Qy        589 GTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAAC 648
Db        364 GAAACAATGCAGCGGGTCGGCGTTCCGACGATTCCGGGCAGTGACGGTCTGCTGACGGAT 423

Qy        649 ATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTT 708
Db        424 GTTGATTCGGCTGCCAAAGTTGCTGCCGAGATCGGCTATCCCGTCATGATCAAAGCGACG 483

Qy        709 GCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTA 768
Db        484 GCGGGGGGCGGTGGTCGCGGTATGCGGCTGGTGCGTGACCCTGCAGATCTGGAAAAACTG 543

Qy        769 GCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAA 828
Db        544 TTCCTTGCTGCCCAAGGAGAAGCCGAGGCAGCTTTTGGGAATCCAGGACTGTATCTCGAA 603

Qy        829 CGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAA 888
Db        604 AAATTTATCGATCGCCCACGCCACGTTGAATTTCAGATCTTGGCCGATGCCTACGGCAAT 663

Qy        889 GTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAA 948
Db        664 GTAGTGCATCTAGGCGAGCGCGATTGCTCCATTCAACGTCGTCACCAAAAGCTGCTCGAA 723

Qy        949 ATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTA 1008
Db        724 GAAGCCCCAGTCCGGCGCTATCGGCAGACCTGCGGCAGAAAATGGGCGATGCCGCCGTC 783

Qy       1009 AAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAA 1068
Db        784 AAAGTCGCTCAAGCGATCGGCTACATCGGTGCCGGCACCGTGGAGTTTCTGGTCGATGCG 843

Qy       1069 AAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACT 1128
Db        844 ACCGGCAACTTCTACTTCATGGAGATGAATACCCGCATCCAAGTCGAGCATCCAGTCACA 903

Qy       1129 GAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACC 1188
Db        904 GAAATGATTACGGGACTGGACTTGATTGCGGAGCAGATTCGGATTGCCCAAGGCG----- 958

Qy       1189 TTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGC 1248
Db        959 ----AAGCGCTGCGCTTCCGGCAAGCCGATATTCAACTGCGCGGCCATGCGATCGAATGC 1014

Qy       1249 CGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCG 1308
Db       1015 CGTATCAATGCGGAAGATCCGGAATACAATTTCCGGCCGAATCCTGGCCGCATTACAGGC 1074

Qy       1309 TACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAA 1368
Db       1075 TATTTACCGCCCGGCGGCCCCGGCGTTCGTGTCGATTCCCATGTTTATACCGACTACGAA 1134

Qy       1369 ATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAA 1428
Db       1135 ATTCCGCCCTATTACGATTCGCTGATTGGCAAATTGATTGTCTGGGGTGCAACACGGGAA 1194

Qy       1429 ACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACC 1488
Db       1195 GAGGCGATCGCGCGGATGCAGCGTGCTCTGCGGGAATGCGCCATCACCGGCTTGCCGACG 1254

Qy       1489 AACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCC 1548
Db       1255 ACCCTTAGTTTCCATCAGCTGATGTTGCAGATGCCTGAGTTCCTGCGCGGGGAACTCTAT 1314

Qy       1549 ACCGGATTCATTG 1561
Db       1315 ACCAACTTTGTTG 1327
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RESULT 14
US-08-475-879-5
; Sequence 5, Application US/08475879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
;   APPLICANT: Robert Haselkorn and Piotr Gornicki
;   TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
;   TITLE OF INVENTION: Carboxylase
;   NUMBER OF SEQUENCES: 116
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: 321 No. 5972644 5786170th Clark Street
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60610
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy Disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII-DOS
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/475,879
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/956,700
;   FILING DATE: 10/21/92
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Thomas E. No. 5972644 5786170thrup
;   REGISTRATION NUMBER: 33,268
;   REFERENCE/DOCKET NUMBER: ARCD:058
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 1-312-744-0090
;   TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1362 base pairs
;   TYPE: Nucleic acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
;   MOLECULE TYPE: Oligonucleotide
US-08-475-879-5

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Query Match            8.6%;  Score 313;  DB 2;  Length 1362;
Best Local Similarity  53.9%;  Pred. No. 5.7e-79;
Matches  718;  Conservative    0;  Mismatches  600;  Indels   15;  Gaps    3;

Qy      232 TTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCA 291
Db        7 TTCAACAAGATCCTGATCGCCAATCGCGGCGAAATCGCCCTGCGCATTCTCCGCACTTGT 66

Qy      292 CTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCAC 351
Db       67 CAAGAACTCGGGATCGGCACGATCGCCGTTCACTCCACTGTGGATCGCAACGCGCTCCAT 126

Qy      352 CGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTAC 411
Db      127 GTGCAGTTAGCGGACGAAGCGGTCTGTATTGG---CGAAGCGGCCAGCAGCAAAAGCTAT 183

Qy      412 CTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCG 471
Db      184 CTCAATATCCCCAACATCATTGCGGCGGCCCTGACCCCTAATGCCAGCGCCATTCACCCC 243

Qy      472 GGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATT 531
Db      244 GGCTATGGCTTCTTGGCGGAGAATGCCCGCTTTGCAGAAATCTGCGCCGATCACCATCTC 303

Qy      532 ACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGC---G 588
Db      304 ACCTTTATTGGCCCCAGCCCCGATTCGATTCGAGCCATGGGCGATAAATCCACCGCTAAG 363

Qy      589 GTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAAC 648
Db      364 GAAACAATGCAGCGGGTCGGCGTTCCGACGATTCCGGGCAGTGACGGTCTGCTGACGGAT 423

Qy      649 ATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTT 708
Db      424 GTTGATTCGGCTGCCAAAGTTGCTGCCGAGATCGGCTATCCCGTCATGATCAAAGCGACG 483

Qy      709 GCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTA 768
Db      484 GCGGGGGGCGGTGGTCGCGGTATGCGGCTGGTGCGTGACCCTGCAGATCTGGAAAAACTG 543

Qy      769 GCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAA 828
Db      544 TTCCTTGCTGCCCAAGGAGAAGCCGAGGCAGCTTTTGGGAATCCAGGACTGTATCTCGAA 603

Qy      829 CGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAA 888
Db      604 AAATTTATCGATCGCCCACGCCACGTTGAATTTCAGATCTTGGCCGATGCCTACGGCAAT 663

Qy      889 GTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAA 948
Db      664 GTAGTGCATCTAGGCGAGCGCGATTGCTCCATTCAACGTCGTCACCAAAAGCTGCTCGAA 723

Qy      949 ATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTA 1008
Db      724 GAAGCCCCCAGTCCGGCGCTATCGGCAGACCTGCGGCAGAAAATGGGCGATGCCGCCGTC 783

Qy     1009 AAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAA 1068
Db      784 AAAGTCGCTCAAGCGATCGGCTACATCGGTGCCGGCACCGTGGAGTTTCTGGTCGATGCG 843

Qy     1069 AAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACT 1128
Db      844 ACCGGCAACTTCTACTTCATGGAGATGAATACCCGCATCCAAGTCGAGCATCCAGTCACA 903

Qy     1129 GAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACC 1188
Db      904 GAAATGATTACGGGACTGGACTTGATTGCGGAGCAGATTCGGATTGCCCAAGGCG----- 958

Qy     1189 TTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGC 1248
Db      959 ----AAGCGCTGCGCTTCCGGCAAGCCGATATTCAACTGCGCGGCCATGCGATCGAATGC 1014

Qy     1249 CGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCG 1308
Db     1015 CGTATCAATGCGGAAGATCCGGAATACAATTTCCGGCCGAATCCTGGCCGCATTACAGGC 1074

Qy     1309 TACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAA 1368
Db     1075 TATTTACCGCCCGGCGGCCCCGGCGTTCGTGTCGATTCCCATGTTTATACCGACTACGAA 1134

Qy     1369 ATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAA 1428
Db     1135 ATTCCGCCCTATTACGATTCGCTGATTGGCAAATTGATTGTCTGGGGTGCAACACGGGAA 1194

Qy     1429 ACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACC 1488
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; Sequence 5, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
;  APPLICANT: HASELKORN, ROBERT
;  APPLICANT:  GORNICKI, PIOTR
;  TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
;  FILE REFERENCE: ARCD:338US
;  CURRENT APPLICATION NUMBER: US/09/433,043B
;  CURRENT FILING DATE:  1999-10-25
;  PRIOR APPLICATION NUMBER: 08/475,879
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/956,700
;  PRIOR FILING DATE: 1992-10-02
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-433-043B-5

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  Best Local Similarity  53.9%;  Pred. No. 5.7e-79;
  Matches  718;  Conservative    0;  Mismatches  600;  Indels   15;  Gaps    3;

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Qy      472 GGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATT 531
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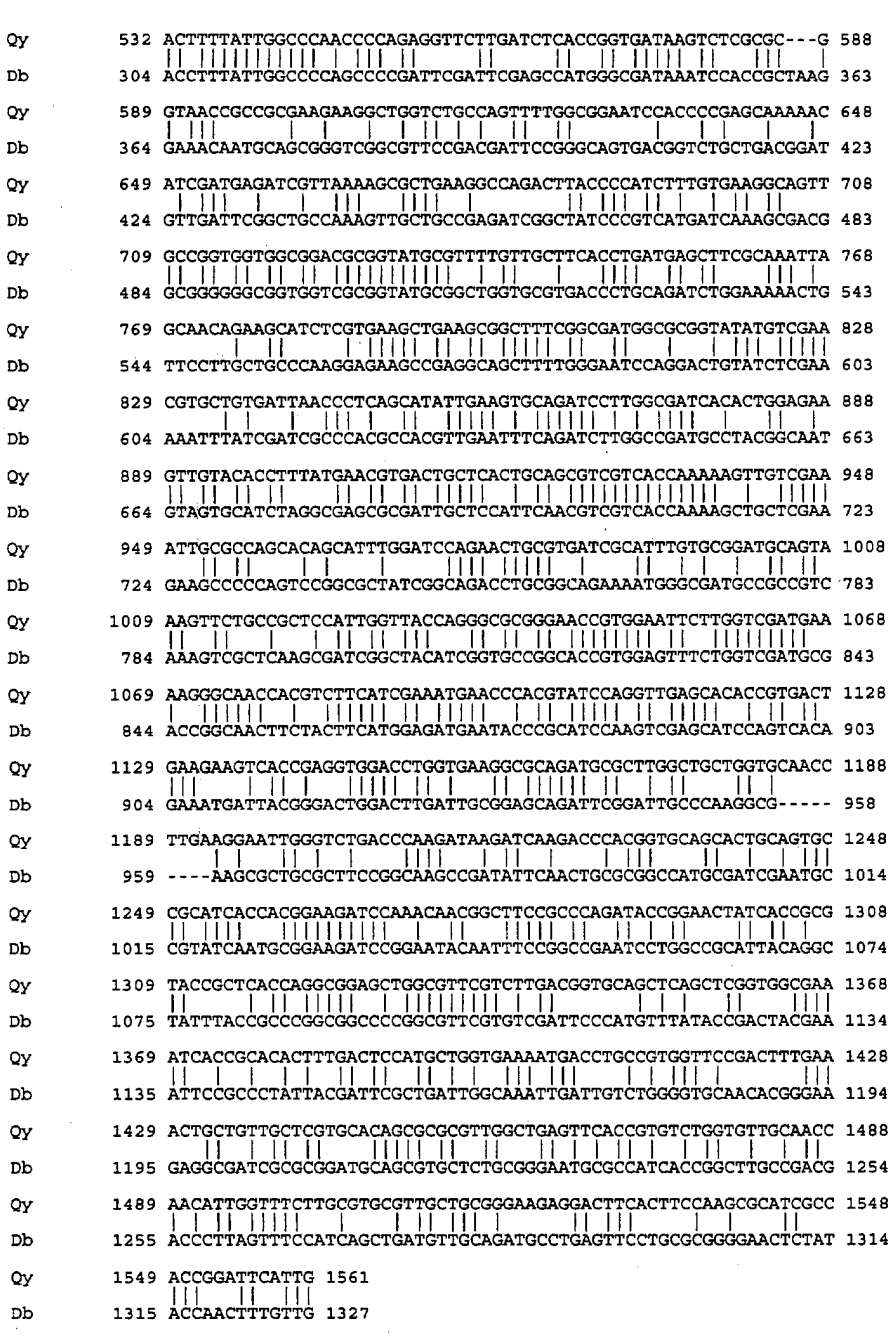

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Job time : 257 secs

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Searched: 2438257 seqs, 1849576744 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	3420	94.4	3420	9	US-09-738-626-765	Sequence 765, App
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ALIGNMENTS

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; Sequence 1, Application US/10045072
; Publication No. US20030027305A1
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790002
; CURRENT APPLICATION NUMBER: US/10/045,072
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 09/677,575
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 09/220,081
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
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US-10-045-072-1

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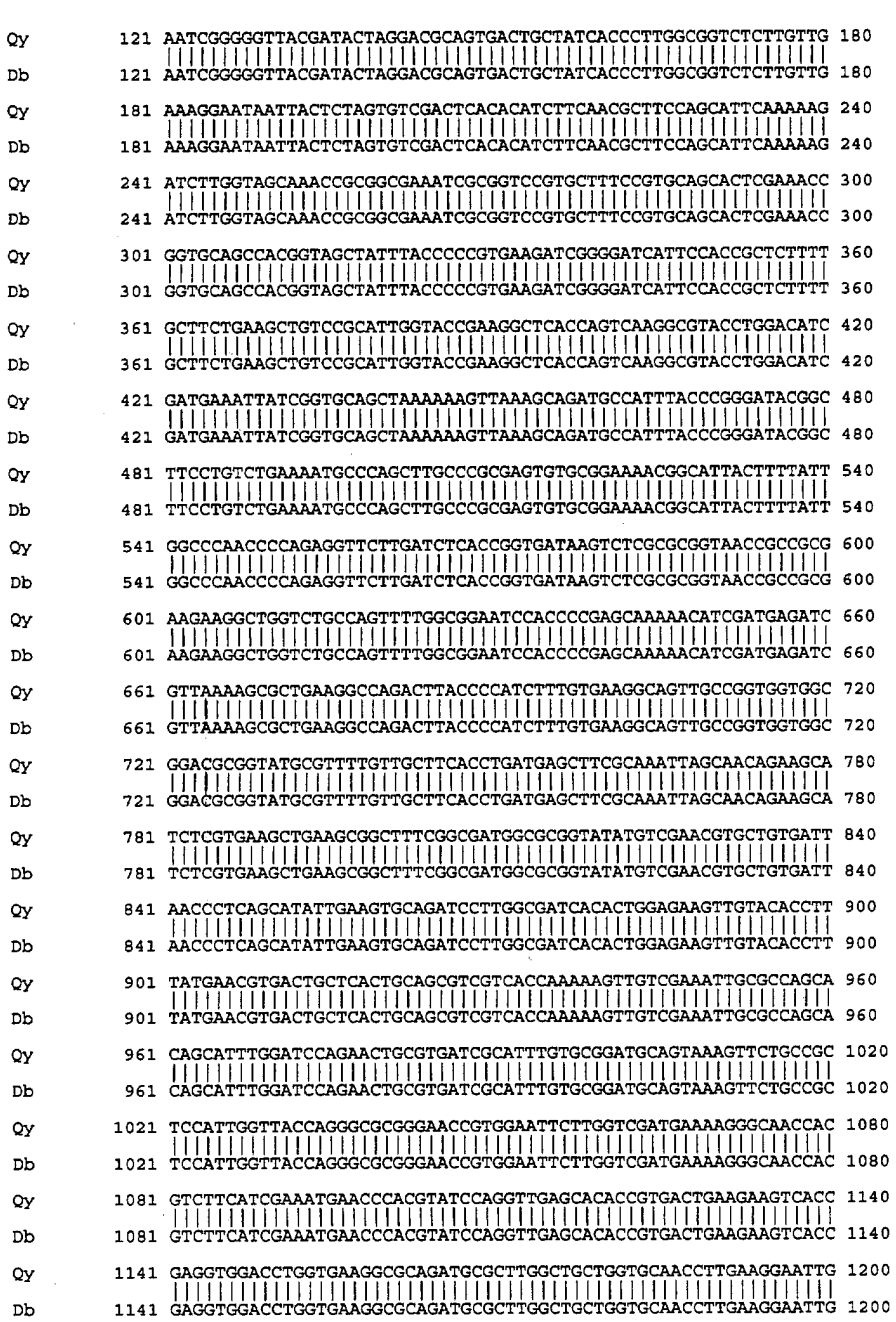
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Qy      3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
Db      3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
Qy      3601 TTGATCGTCGTCGTTTCCTAA 3621
Db      3601 TTGATCGTCGTCGTTTCCTAA 3621
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RESULT 2
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 100.0%; Score 3621; DB 9; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      705013 TGGGGCGGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 705072
Qy          61 TCAGGGGAGTGTTGCCCGAAAACATTGAGAGGAAAACAAAAACCGATGTTTGATTGGGGG 120
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Qy         121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 180
Db      705133 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCTTGGCGGTCTCTTGTTG 705192
Qy         181 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
Db      705193 AAAGGAATAATTACTCTAGTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 705252
Qy         241 ATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 300
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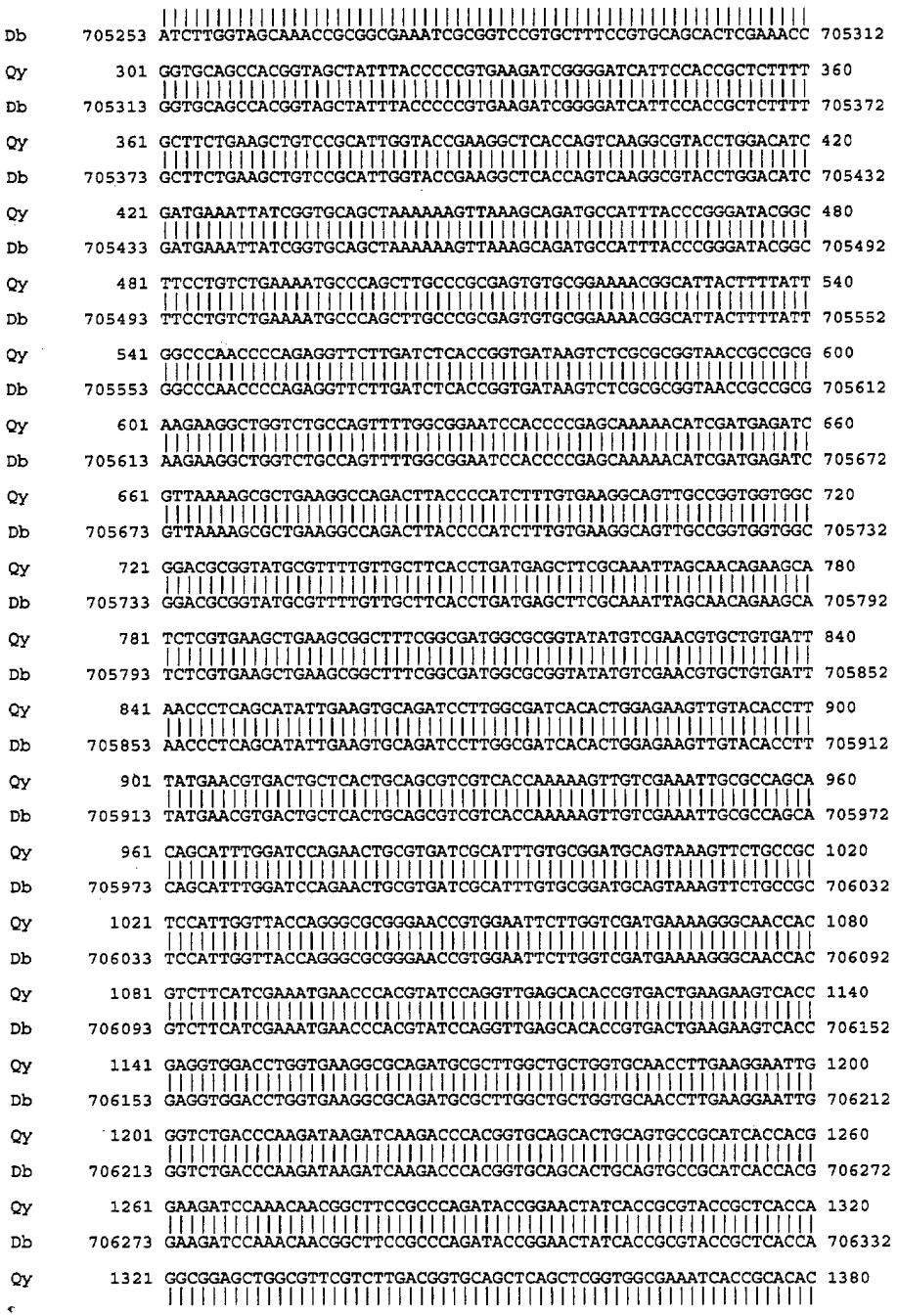
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Db 705313 GGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 705372
Qy 361 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 420
Db 705373 GCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATC 705432
Qy 421 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
Db 705433 GATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 705492
Qy 481 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 540
Db 705493 TTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATT 705552
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Db 705553 GGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCG 705612
Qy 601 AAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 660
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Qy 661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
Db 705673 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 705732
Qy 721 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
Db 705733 GGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 705792
Qy 781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 840
Db 705793 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATT 705852
Qy 841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
Db 705853 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 705912
Qy 901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960
Db 705913 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 705972
Qy 961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
Db 705973 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 706032
Qy 1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080
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Qy 1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
Db 706093 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 706152
Qy 1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
Db 706153 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 706212
Qy 1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
Db 706213 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 706272
Qy 1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
Db 706273 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 706332
Qy 1321 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 1380
Db 706333 GGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACAC 706392
Qy 1381 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 1440
Db 706393 TTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 706452
Qy 1441 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 1500
Db 706453 CGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTC 706512
Qy 1501 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560
Db 706513 TTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 706572
Qy 1561 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 1620
Db 706573 GCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTG 706632
Qy 1621 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
Db 706633 GATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 706692
Qy 1681 GCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740
Db 706693 GCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 706752
Qy 1741 CGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTG 1800
Db 706753 CGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTG 706812
Qy 1801 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 1860
Db 706813 GCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGC 706872
Qy 1861 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 1920
Db 706873 TCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCC 706932
Qy 1921 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
Db 706933 GTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 706992
Qy 1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
Db 706993 TGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 707052
Qy 2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 2100
Db 707053 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTT 707112
Qy 2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 2160
Db 707113 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTC 707172
Qy 2161 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 2220
Db 707173 TCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTG 707232
Qy 2221 GCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTAC 2280
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Qy 2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 2340
Db 707293 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGAT 707352
Qy 2341 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
Db 707353 ATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAA 707412
Qy 2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 2460
Db 707413 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTAC 707472

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Qy       2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 2520
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Db     707473 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGC 707532

Qy       2521 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     707533 ACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGAT 707592

Qy       2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 2640
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Db     707593 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGA 707652

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Qy       2701 ATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGAT 2760
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Qy       2821 AAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGT 2880
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Qy       2881 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 2940
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Db     707893 GTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATC 707952

Qy       2941 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
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Db     707953 GCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 708012

Qy       3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 3060
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Db     708013 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAG 708072

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Db     708073 CAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTG 708132

Qy       3121 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 3180
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Db     708133 TTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCG 708192

Qy       3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 3240
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Db     708193 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTG 708252

Qy       3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     708253 CCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAG 708312

Qy       3301 GGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
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Qy       3421 GTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
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Qy       3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
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Db     708493 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 708552

Qy       3541 GTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGAC 3600
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RESULT 3
US-09-738-626-765
; Sequence 765, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 765
; LENGTH: 3420
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-765

Query Match 94.4%; Score 3420; DB 9; Length 3420;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        199 GTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGC 258
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Db          1 GTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGC 60

Qy        259 GGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCT 318
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Qy        319 ATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGC 378
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Db        121 ATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGC 180

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Db        181 ATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCA 240

Qy        439 GCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCC 498
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Db        241 GCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCC 300

Qy        499 CAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTT 558
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Db        301 CAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTT 360

Qy        559 CTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCA 618
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Db        421 GTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATCGTTAAAAGCGCTGAAGGC 480

Qy        679 CAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTT 738
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Qy        739 GTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCG 798
Db        541 GTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCG 600

Qy        799 GCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAA 858
Db        601 GCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAA 660

Qy        859 GTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCA 918
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Qy        919 CTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAA 978
Db        721 CTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAA 780

Qy        979 CTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGC 1038
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Qy       1039 GCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAAC 1098
Db        841 GCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAAC 900

Qy       1099 CCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAG 1158
Db        901 CCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAG 960

Qy       1159 GCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAG 1218
Db        961 GCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAG 1020

Qy       1219 ATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGC 1278
Db       1021 ATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGC 1080

Qy       1279 TTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGT 1338
Db       1081 TTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGT 1140

Qy       1339 CTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTG 1398
Db       1141 CTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTG 1200

Qy       1399 AAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTG 1458
Db       1201 AAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTG 1260

Qy       1459 GCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGG 1518
Db       1261 GCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGG 1320

Qy       1519 GAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATTGCCGATCACCCGCACCTC 1578
Db       1321 GAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATTGCCGATCACCCGCACCTC 1380

Qy       1579 CTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTC 1638
Db       1381 CTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTC 1440

Qy       1639 ACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTG 1698
Db       1441 ACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTG 1500

Qy       1699 CCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGC 1758
Db       1501 CCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGC 1560

Qy       1759 CCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACC 1818
Db       1561 CCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACC 1620

Qy       1819 TTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCT 1878
Db       1621 TTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCT 1680

Qy       1879 GCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGC 1938
Db       1681 GCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGC 1740

Qy       1939 GCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAG 1998
Db       1741 GCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAG 1800

Qy       1999 CTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTG 2058
Db       1801 CTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTG 1860

Qy       2059 GGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCC 2118
Db       1861 GGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCC 1920

Qy       2119 GGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCA 2178
Db       1921 GGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCA 1980

Qy       2179 ATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGT 2238
Db       1981 ATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGT 2040

Qy       2239 GATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAG 2298
Db       2041 GATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAG 2100

Qy       2299 GAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGATATGGCTGGTCTGCTTCGC 2358
Db       2101 GAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGATATGGCTGGTCTGCTTCGC 2160

Qy       2359 CCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCAC 2418
Db       2161 CCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCAC 2220

Qy       2419 GTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCT 2478
Db       2221 GTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCT 2280

Qy       2479 GGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCC 2538
Db       2281 GGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCC 2340

Qy       2539 CTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAG 2598
Db       2341 CTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAG 2400

Qy       2599 GCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAG 2658
Db       2401 GCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAG 2460

Qy       2659 TCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTG 2718
Db       2461 TCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTG 2520

Qy       2719 TCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGATCGTTTCGAACTCATCGAA 2778
Db       2521 TCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCGGATCGTTTCGAACTCATCGAA 2580

Qy       2779 GACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCC 2838
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Db       2581 GACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCC 2640

Qy       2839 AAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGTGTGGATCCAGCAGACTTT 2898

Db       2641 AAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGTGTGGATCCAGCAGACTTT 2700

Qy       2899 GCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAG 2958

Db       2701 GCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAG 2760

Qy       2959 CTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGGCCGC 3018

Db       2761 CTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGGCCGC 2820

Qy       3019 TCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCT 3078

Db       2821 TCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCT 2880

Qy       3079 GATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAA 3138

Db       2881 GATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAA 2940

Qy       3139 GAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTC 3198

Db       2941 GAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTC 3000

Qy       3199 TTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCA 3258

Db       3001 TTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCA 3060

Qy       3259 CTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTG 3318

Db       3061 CTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTG 3120

Qy       3319 GCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTC 3378

Db       3121 GCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTC 3180

Qy       3379 ACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCT 3438

Db       3181 ACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCT 3240

Qy       3439 GGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCA 3498

Db       3241 GGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCA 3300

Qy       3499 ATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAAATCGAT 3558

Db       3301 ATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAAATCGAT 3360

Qy       3559 CGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCC 3618

Db       3361 CGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCC 3420
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RESULT 4
US-09-974-973-1
; Sequence 1, Application US/09974973
; Patent No. US20020177202A1
; GENERAL INFORMATION:
; APPLICANT: Hanke, Paul D.
; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacterium
; FILE REFERENCE: 1533.1230001/MAC/RGM
; CURRENT APPLICATION NUMBER: US/09/974,973
; CURRENT FILING DATE: 2001-10-21
; PRIOR APPLICATION NUMBER: US 60/239,913
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3474
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3474)
US-09-974-973-1

Query Match 93.9%; Score 3398.8; DB 9; Length 3474;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 3427; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy        148 GTGACTGCTATCACCCTTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACT 207

Db          1 GTGACTGCTATCACCCTTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACT 60

Qy        208 CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATC 267

Db         61 CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATC 120

Qy        268 GCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC 327

Db        121 GCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC 180

Qy        328 CGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACC 387

Db        181 CGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACT 240

Qy        388 GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA 447

Db        241 GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA 300

Qy        448 GTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCC 507

Db        301 GTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCCTGTCTGAAAATGCCCAGCTTGCC 360

Qy        508 CGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTC 567

Db        361 CGCGAGTGCGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTC 420

Qy        568 ACCGGTGATAAGTCTCGCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCG 627

Db        421 ACCGGTGATAAGTCTCGTGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCG 480

Qy        628 GAATCCACCCCGAGCAAAAACATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTAC 687

Db        481 GAATCCACCCCGAGCAAAAACATCGATGACATCGTTAAAAGCGCTGAAGGCCAGACTTAC 540

Qy        688 CCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCA 747

Db        541 CCCATCTTTGTAAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGCTTTGTTTCTTCA 600

Qy        748 CCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGC 807

Db        601 CCTGATGAGCTCCGCAAATTGGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCATTCGGC 660

Qy        808 GATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATC 867

Db        661 GACGGTTCGGTATATGTCGAACGTGCTGTGATTAACCCCCAGCACATTGAAGTGCAGATC 720

Qy        868 CTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 927

Db        721 CTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 780

Qy        928 CGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGAT 987

Db        781 CGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGAT 840

Qy        988 CGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACC 1047

Db        841 CGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACC 900

Qy       1048 GTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATC 1107

Db        901 GTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTTTTCATCGAAATGAACCCACGTATC 960
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Qy   1108 CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG 1167
Db    961 CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG 1020

Qy   1168 CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC 1227
Db   1021 CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC 1080

Qy   1228 CACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCA 1287
Db   1081 CACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCA 1140

Qy   1288 GATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGT 1347
Db   1141 GATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGT 1200

Qy   1348 GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACC 1407
Db   1201 GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACC 1260

Qy   1408 TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTC 1467
Db   1261 TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTC 1320

Qy   1468 ACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC 1527
Db   1321 ACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC 1380

Qy   1528 TTCACTTCCAAGCGCATCGCCACCGGATTCATTGCCGATCACCCGCACCTCCTTCAGGCT 1587
Db   1381 TTCACTTCCAAGCGCATCGCCACCGGATTTATCGGCGATCACCCACACCTCCTTCAGGCT 1440

Qy   1588 CCACCTGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC 1647
Db   1441 CCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC 1500

Qy   1648 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATC 1707
Db   1501 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCAATCGATAAGCTGCCCAACATC 1560

Qy   1708 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG 1767
Db   1561 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG 1620

Qy   1768 TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT 1827
Db   1621 TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT 1680

Qy   1828 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG 1887
Db   1681 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG 1740

Qy   1888 GCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTAC 1947
Db   1741 GCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTAC 1800

Qy   1948 GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 2007
Db   1801 GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 1860

Qy   2008 GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC 2067
Db   1861 GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC 1920

Qy   2068 CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC 2127
Db   1921 CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC 1980

Qy   2128 ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCA 2187
Db   1981 ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCA 2040

Qy   2188 GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCT 2247
Db   2041 GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCT 2100

Qy   2248 GATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC 2307
Db   2101 GATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC 2160

Qy   2308 AAGTCTGGCGCTCACATCTTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCG 2367
Db   2161 AAGTCTGGCGCTCACATTCTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCG 2220

Qy   2368 GTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACACC 2427
Db   2221 GTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACACC 2280

Qy   2428 CACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGCAGAT 2487
Db   2281 CACGACACTGCGGGTGGCCAGTTGGCTACCTACTTTGCTGCAGCTCAAGCTGGTGCAGAT 2340

Qy   2488 GCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCC 2547
Db   2341 GCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCC 2400

Qy   2548 ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT 2607
Db   2401 ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT 2460

Qy   2608 GACCTCGAGCCGTACTGGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2667
Db   2461 GACCTCGAGCCGTACTGGGAAGCTGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2520

Qy   2668 CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG 2727
Db   2521 CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG 2580

Qy   2728 CGTGCACAGGCCACCGCACTGGGCCTTGCGGATCGTTTCGAACTCATCGAAGACAACTAC 2787
Db   2581 CGTGCACAGGCCACCGCACTGGGCCTTGCTGATCGCTTCGAGCTCATCGAAGACAACTAC 2640

Qy   2788 GCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTT 2847
Db   2641 GCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTT 2700

Qy   2848 GGCGACCTCGCACTCCACCTCGTTGGTGCGGGTGTGGATCCAGCAGACTTTGCTGCCGAT 2907
Db   2701 GGCGACCTCGCACTCCACCTGGTTGGTGCGGGTGTAGATCCAGCAGACTTTGCTGCAGAC 2760

Qy   2908 CCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAAC 2967
Db   2761 CCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAAC 2820

Qy   2968 CCTCCAGGTGGCTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC 3027
Db   2821 CCTCCAGGTGGCTGGCCAGAACCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC 2880

Qy   3028 AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC 3087
Db   2881 AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC 2940

Qy   3088 AAGGAACGTCGCAATAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTC 3147
Db   2941 AAGGAACGTCGCAACAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTC 3000

Qy   3148 GAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGC 3207
Db   3001 GAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGA 3060

Qy   3208 CTGGTCGAAGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT 3267
Db   3061 CTGGTCGAGGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT 3120

Qy   3268 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC 3327
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Db       3121 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC 3180

Qy       3328 AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACC 3387

Db       3181 AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACC 3240

Qy       3388 GCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTC 3447

Db       3241 GCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTC 3300

Qy       3448 ACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG 3507

Db       3301 ACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG 3360

Qy       3508 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAAATCGATCGCGTTGTG 3567

Db       3361 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATTGAACGCGTTGTG 3420

Qy       3568 GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA 3621

Db       3421 GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA 3474


RESULT 5
US-09-974-973-3
; Sequence 3, Application US/09974973
; Patent No. US20020177202A1
; GENERAL INFORMATION:
;  APPLICANT: Hanke, Paul D.
;  TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacterium
;  FILE REFERENCE: 1533.1230001/MAC/RGM
;  CURRENT APPLICATION NUMBER: US/09/974,973
;  CURRENT FILING DATE:  2001-10-21
;  PRIOR APPLICATION NUMBER: US 60/239,913
;  PRIOR FILING DATE: 2000-10-13
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 3474
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-974-973-3

  Query Match             93.9%;  Score 3398.8;  DB 9;  Length 3474;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 3427;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy        148 GTGACTGCTATCACCCTTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACT 207

Db          1 GTGACTGCTATCACCCTTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACT 60

Qy        208 CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATC 267

Db         61 CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATC 120

Qy        268 GCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC 327

Db        121 GCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC 180

Qy        328 CGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACC 387

Db        181 CGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACT 240

Qy        388 GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA 447

Db        241 GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA 300

Qy        448 GTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCC 507

Db        301 GTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCCTGTCTGAAAATGCCCAGCTTGCC 360

Qy        508 CGCGAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTC 567

Db        361 CGCGAGTGCGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTC 420

Qy        568 ACCGGTGATAAGTCTCGCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCG 627

Db        421 ACCGGTGATAAGTCTCGTGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCG 480

Qy        628 GAATCCACCCCGAGCAAAAACATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTAC 687

Db        481 GAATCCACCCCGAGCAAAAACATCGATGACATCGTTAAAAGCGCTGAAGGCCAGACTTAC 540

Qy        688 CCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCA 747

Db        541 CCCATCTTTGTAAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGCTTTGTTTCTTCA 600

Qy        748 CCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGC 807

Db        601 CCTGATGAGCTCCGCAAATTGGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCATTCGGC 660

Qy        808 GATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATC 867

Db        661 GACGGTTCGGTATATGTCGAACGTGCTGTGATTAACCCCCAGCACATTGAAGTGCAGATC 720

Qy        868 CTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 927

Db        721 CTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 780

Qy        928 CGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGAT 987

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Qy       1048 GTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATC 1107

Db        901 GTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTTTTCATCGAAATGAACCCACGTATC 960

Qy       1108 CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG 1167

Db        961 CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG 1020

Qy       1168 CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC 1227

Db       1021 CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC 1080

Qy       1228 CACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCA 1287

Db       1081 CACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCA 1140

Qy       1288 GATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGT 1347

Db       1141 GATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGT 1200

Qy       1348 GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACC 1407

Db       1201 GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACC 1260

Qy       1408 TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTC 1467

Db       1261 TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTC 1320

Qy       1468 ACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC 1527

Db       1321 ACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC 1380

Qy       1528 TTCACTTCCAAGCGCATCGCCACCGGATTCATTGCCGATCACCCGCACCTCCTTCAGGCT 1587

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Qy       1588 CCACCTGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC 1647
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Db      1441 CCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC 1500
Qy      1648 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATC 1707
Db      1501 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCAATCGATAAGCTGCCCAACATC 1560
Qy      1708 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG 1767
Db      1561 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG 1620
Qy      1768 TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT 1827
Db      1621 TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT 1680
Qy      1828 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG 1887
Db      1681 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG 1740
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Qy      1948 GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 2007
Db      1801 GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 1860
Qy      2008 GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC 2067
Db      1861 GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC 1920
Qy      2068 CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC 2127
Db      1921 CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC 1980
Qy      2128 ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCA 2187
Db      1981 ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCA 2040
Qy      2188 GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCT 2247
Db      2041 GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCT 2100
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Qy      2308 AAGTCTGGCGCTCACATCTTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCG 2367
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Qy      2368 GTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACACC 2427
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Qy      2428 CACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGCAGAT 2487
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Qy      2488 GCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCC 2547
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Db      2401 ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT 2460
Qy      2608 GACCTCGAGCCGTACTGGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2667
Db      2461 GACCTCGAGCCGTACTGGGAAGCTGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2520
Qy      2668 CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG 2727
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Qy      2728 CGTGCACAGGCCACCGCACTGGGCCTTGCGGATCGTTTCGAACTCATCGAAGACAACTAC 2787
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Qy      2788 GCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTT 2847
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Qy      2848 GGCGACCTCGCACTCCACCTCGTTGGTGCGGGTGTGGATCCAGCAGACTTTGCTGCCGAT 2907
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Db      2821 CCTCCAGGTGGCTGGCCAGAACCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC 2880
Qy      3028 AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC 3087
Db      2881 AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC 2940
Qy      3088 AAGGAACGTCGCAATAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTC 3147
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Qy      3208 CTGGTCGAAGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT 3267
Db      3061 CTGGTCGAGGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT 3120
Qy      3268 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC 3327
Db      3121 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC 3180
Qy      3328 AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACC 3387
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Qy      3448 ACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG 3507
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RESULT 6
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; Sequence 17701, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith

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;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17701
;   LENGTH: 3423
;   TYPE: DNA
;   ORGANISM: Cornyebacterium diptheriae
US-10-282-122A-17701

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  Matches 2494;  Conservative    0;  Mismatches  896;  Indels    9;  Gaps    2;

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Qy        273 CCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGA 332
Db         87 GCGAGCTTTTCGTGCAGCCTTTGAAACCGGTGCTGCCACGGTAGCTGTCTACCCGAACGA 146

Qy        333 AGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGG 392
Db        147 AGACCGTAATTCATTCCACCGATCGTTTGCCTCTGAAGCTGTCCTCATTGGTGAGGGCGG 206

Qy        393 CTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAA 452
Db        207 ATCTGCGGTCAAAGCGTACCTCGATATCGACGAAATCATCCGTGCTGCTAAACAAACGGG 266

Qy        453 AGCAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGA 512
Db        267 TGCCGACGCAATTTACCCAGGCTACGGCTTCCTTTCCGAAAACGCCCAGCTTGCTCGTGA 326

Qy        513 GTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGG 572
Db        327 GTGCGCTGAAAACGGCATAACCTTTATCGGTCCACCTCCATCAGTGCTGGAGCTTACCGG 386

Qy        573 TGATAAGTCTCGCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATC 632
Db        387 TGATAAAGCAGCTGCTGTTACCGCAGCACGCGAGGCAGGTTTGCCCACGCTGACTGAGAC 446

Qy        633 CACCCCGAGCAAAAACATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCAT 692

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Qy        693 CTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGA 752
Db        507 ATTCGTCAAAGCCGTTGCCGGTGGTGGTGGCCGCGGCATGCGTTTTGTCGACGCCCCCGA 566

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Qy        873 CGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTCA 932
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Db        807 TTGTGCAGACGCAGTCGCGTTTGCACGCCACATCGGTTACCAAGGTGCAGGCACGGTCGA 866

Qy       1053 ATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGT 1112
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Db        927 CGAACACACCGTGACCGAAGAGGTCACCCAAGTCGACTTGGTGAAGTCCCAGATCATGAT 986

Qy       1173 GGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGG 1232
Db        987 CGCCTCCGGTGCGACACTCGAAGATCTCGGTCTGCGCCAAGAAGACATCCACACCGAAGG 1046

Qy       1233 TGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATAC 1292
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Qy       1293 CGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGC 1352
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Qy       1353 TCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCG 1412
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Qy       1413 TGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGT 1472
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Qy       1473 GTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCAC 1532
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Qy       1533 TTCCAAGCGCATCGCCACCGGATTCATTGCCGATCACCCGCACCTCCTTCAGGCTCCACC 1592
Db       1347 GCACAAGCGCATCGCCACTGGCTTCATCGCAGATCACCCATGGCTGCTGCAGGCACCACC 1406

Qy       1593 TGCTGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAACAAGCC 1652
Db       1407 TGCCGACGATGAGCCTGGCCGCATTTTGAACTACCTAGCTGATGTGACTGTGAACAAGCC 1466

Qy       1653 TCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATCAAGGA 1712
Db       1467 TCATGGTCTACGCCCA---GCCGTGATCAACCCGGTAGAAAAGCTCCCAGCAGAGATCAA 1523

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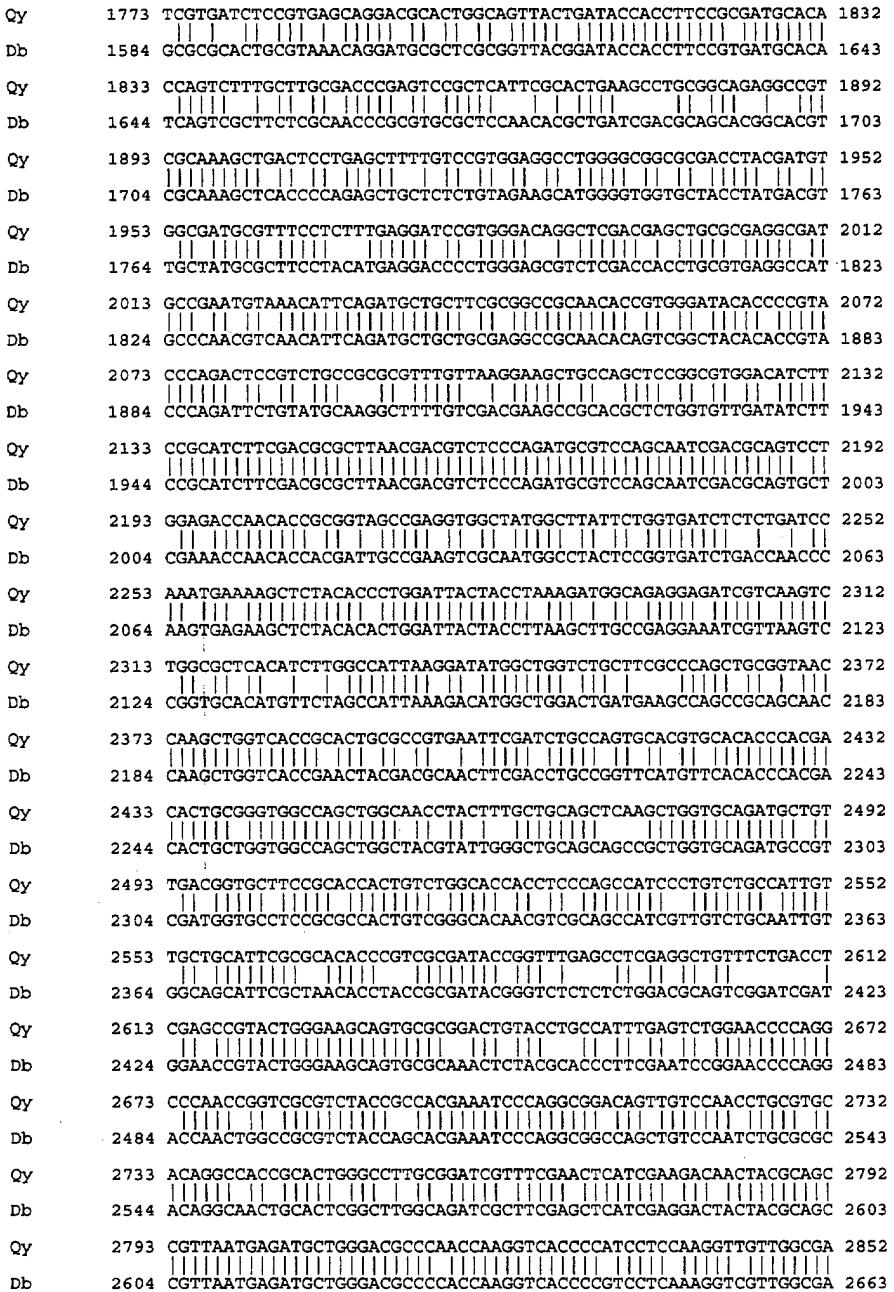

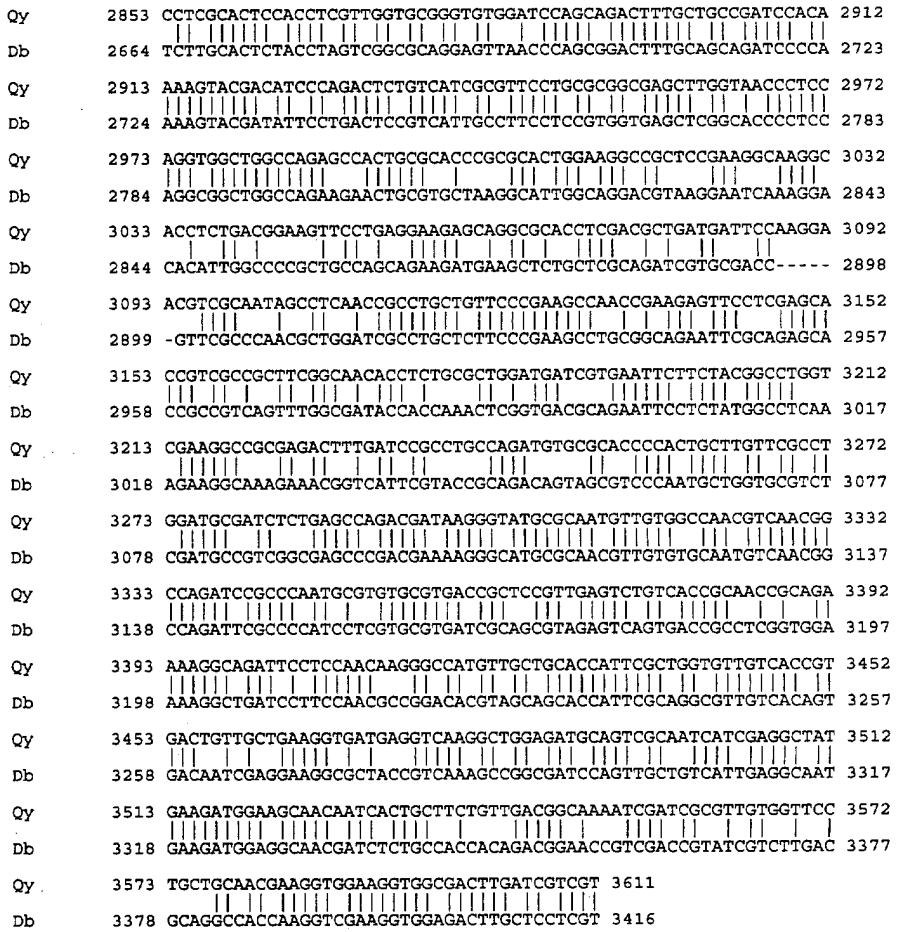

RESULT 7
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; Sequence 25766, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A

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;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25766
;   LENGTH: 3381
;   TYPE: DNA
;   ORGANISM: Mycobacterium avium
US-10-282-122A-25766

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  Best Local Similarity   63.2%;  Pred. No. 0;
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Qy        598 GCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAG 657
Db        370 GCGCGGGCCGCGGGTCTTCCGGTGCTGGCCTCCTCGCCGCCGTCGACCTCGGTGCAGGAG 429

Qy        658 ATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGT 717
Db        430 TTGCTGAGCGCCGCCGAGACGATGACGTTCCCGCTGTTCGTCAAGGCGGTCGCCGGCGGC 489

Qy        718 GGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAA 777
Db        490 GGCGGCCGGGGGATGCGCCGGGTCACCGATCCGGGGGCGCTGGCCGAGGCGATCGAGGCG 549

Qy        778 GCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTG 837
Db        550 GCCAGCCGTGAGGCCGAGTCCGCGTTCGGGGACGCCTCGGTGTTTCTCGAGCAGGCGGTG 609

Qy        838 ATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACAC 897
Db        610 ATCAATCCGCGGCACATCGAGGTCCAGATCCTGGCCGACACGCACGGCAACGTGATGCAC 669

Qy        898 CTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCA 957
Db        670 CTCTACGAGCGGGACTGCAGCGTGCAGCGCCGGCACCAGAAGGTGATCGAGATCGCCCCG 729

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Qy       1078 CACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTC 1137
Db        850 CACGTGTTCATCGAGATGAACCCGCGCATCCAGGTGGAGCACACGGTGACCGAGGAGATC 909

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Qy       1318 CCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCA 1377
Db        1090 CCGGGTGGCGCGGGCATCCGGCTGGACGGCGGCACCACGCTGGGCGCGGAGATCAGCGCG 1149

Qy       1378 CACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTT 1437
Db        1150 CACTTCGATTCGATGCTGATCAAGCTGACCTGCCGGGGACGCGACTTCCCCACGGCGGTG 1209

Qy       1438 GCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGT 1497
Db        1210 CGGCGGGCGCGGCGCGGTCGCCGAATTCCGCATCCGCGGCGTCTCGACGAATATCCCG 1269

Qy       1498 TTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTC 1557
Db        1270 TTCCTGCAAGCGGTTCTGGACGACCCGGATTTTCAGGCTGGGCGCATCACCACCTCGTTC 1329

Qy       1558 ATTGCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATC 1617
Db        1330 ATCGAACAGCGGCCGCAGTTGCTCACCGCGCGCAGTTCGGCCGACCGCGGCACCAAGATC 1389

Qy       1618 CTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTT 1677
Db        1390 CTCAACTACCTGGCCGACGTGACCGTCAACAAGCCGCACGGCGAGCGCCCGTCGGCGGTG 1449

Qy       1678 GCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGT 1737
Db        1450 TACCCGCATGACAAGCTGCCCGACATCGACCTGGCGGCGAGCCCGCCGGCGGGCTCCAAG 1509

Qy       1738 GACCGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCA 1797
Db        1510 CAGCGGTTGACCGAACTCGGGCCGGAGCGATTCGCGGCCTGGCTGCGCGAGTCGGGCGGC 1569

Qy       1798 CTGGCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTC 1857
Db        1570 GTCGGCGTCACCGACACCACGTTCCGCGACGCGCACCAGTCGCTGCTGGCGACCCGGGTC 1629

Qy       1858 CGCTCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTG 1917
Db        1630 CGCACCAGCGGGCTGCTCAAGGTGGCACCCTACATCGCACGGACCATGCCGCAGCTGTTG 1689
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Qy      1918 TCCGTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGAT 1977
Db      1690 TCGGTGGAGTGTTGGGGCGGAGCGACTTACGACGTGGCGCTGCGGTTTCTCAAGGAGGAC 1749

Qy      1978 CCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTG 2037
Db      1750 CCGTGGGAGCGGCTGACGGCGCTGCGCGAGGCGATGCCGAACATCTGCCTTCAGATGCTG 1809

Qy      2038 CTTCGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTT 2097
Db      1810 CTGCGTGGGCGTAACACCGTGGGGTACACGCCCTATCCGGAGACGGTCACGACGGCCTTC 1869

Qy      2098 GTTAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGAC 2157
Db      1870 GTCGCGGAGGCGACCGAGACCGGCATCGACATCTTCCGCATCTTCGACGCGTTGAACAAC 1929

Qy      2158 GTCTCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAG 2217
Db      1930 GTCGACTCGATGCGCCCGGCCATCGACGCGGTCCGCGAAACCGGAAGCGCCATAGCCGAA 1989

Qy      2218 GTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGAT 2277
Db      1990 GTGGCGATGTCCTACACCGGCGACCTGTCCGATCCGGCCGAAAAGCTTTACACGCTGGAC 2049

Qy      2278 TACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAG 2337
Db      2050 TATTACCTGAAGCTGGCCGACCAGATCGTCGAAGCGGGCGCGCACGTGCTGGCGATCAAG 2109

Qy      2338 GATATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGT 2397
Db      2110 GACATGGCCGGCCTGCTGCGCGCACCGGCGGCCGCGACGCTGGTGTCGGCGCTGAAGTCG 2169

Qy      2398 GAATTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACC 2457
Db      2170 CGGTTCGACCTGCCGGTGCACGTGCACACCCATGACACGCCGGGCGGACAGCTGGCGACC 2229

Qy      2458 TACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCT 2517
Db      2230 TACGTGGCGGCCTGGCAGGCCGGGGCCGATGCGGTCGACGGCGCCGCCGCGCCGCTCGCC 2289

Qy      2518 GGCACCACCTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCCGTCGC 2577
Db      2290 GGAACCACCAGCCAGCCGGCACTATCGTCGATCGTGGCCGCCGCGGCCAACACGGAGTAT 2349

Qy      2578 GATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGC 2637
Db      2350 GACACCGGGTTGTCCCTGCCGGCGGTGTGCGATCTGGAGCCGTACTGGGAGGCGCTGCGA 2409

Qy      2638 GGACTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCAC 2697
Db      2410 AAGGTATACGCTCCCTTCGAATCCGGTCTTCCGGCGCCGACCGGGCGGGTGTATCACCAC 2469

Qy      2698 GAAATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTGGGCCTTGCG 2757
Db      2470 GAGATCCCGGGCGGCCAATTGTCGAATCTGCGTCAGCAGGCGATTGCGCTGGGACTCGGC 2529

Qy      2758 GATCGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCA 2817
Db      2530 GACCGGTTCGAGGACATCGAAAACGCCTACGCCGGCGCCGACGCGATTTTGGGACACCTG 2589

Qy      2818 ACCAAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCG 2877
Db      2590 GTCAAGGTCACACCGTCCAGCAAGGTGGTGGGCGACCTGGCGCTGGCCCTGGTGGGTGCG 2649

Qy      2878 GGTGTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTC 2937
Db      2650 GGTGTGGGCGCGCAGGACTTCGCCGAAGACCCCTCCCGCTACGACATCCCGGATTCGGTG 2709

Qy      2938 ATCGCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGC 2997
Db      2710 ATCGGCTTTCTGCGCGGCGAGCTCGGTGACCCGCCGGGCGGCTGGCCGGAGCCGTTGCGC 2769

Qy      2998 ACCCGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAA 3057
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Db      2770 ACCAAGGCCTTACAGGGCCGGGGGCCGGCCAAGCCGGAGCAGCCGCTGACGGCCGAGGAC 2829

Qy      3058 GAGCAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTG 3117
Db      2830 GAAGCGGCGTTGGCCGCCCCGGGTG------CGCGACGGCAGGCAGCGCTGAACCGGCTG 2883

Qy      3118 CTGTTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCT 3177
Db      2884 CTGTTCCCGGGACCGACCAAGGAGCTCGAGGAGCACCGCGAGCAGTACGGTGACACCTCG 2943

Qy      3178 GCGCTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATCCGC 3237
Db      2944 GGGCTGAGCGCCAACCAGTTCTTCTACGGATTGCGGCAGGGCGACGAACACCGCGTCGAA 3003

Qy      3238 CTGCCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGAT 3297
Db      3004 CT---CGAGCGCGGCGTGGAGTTGCTGATCGGCCTGGAGGCCATCTCCGATCCCGACGAA 3060

Qy      3298 AAGGGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGT 3357
Db      3061 CGCGGCATGCGCACCGTGATGTGCATTCTCAACGGGCAGCTGCGGCCGGTGGTGGTGCGC 3120

Qy      3358 GACCGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGC 3417
Db      3121 GACCGCAGCATCGCCATCGACGTGCCCGCCGCCGAGAAGGCCGACCGCGCCAACCCGGAC 3180

Qy      3418 CATGTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTC 3477
Db      3181 CACATCGCTGCCCCGTTCGCCGGGGTGGTGACGGTCGCCGCCGAGGTCGGCCGGCAGGTC 3240

Qy      3478 AAGGCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCT 3537
Db      3241 GAGGCCGGCCAGACCATCGCGACGATCGAGGCGATGAAGATGGAAGCCGCGGTCACCAGC 3300

Qy      3538 TCTGTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGC 3597
Db      3301 CCGAAGTCGGGCAAGGTGGCGCGAATCGCCGTGTCGCGGACCGCTCAAGTCGAGGGCGGC 3360

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RESULT 8
US-10-282-122A-28626
; Sequence 28626, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06

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;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28626
;   LENGTH: 3384
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28626

  Query Match             35.7%;  Score 1294.4;  DB 12;  Length 3384;
  Best Local Similarity   62.0%;  Pred. No. 0;
  Matches 2099;  Conservative    0;  Mismatches 1276;  Indels    9;  Gaps    3;

Qy        238 AAGATCTTGGTAGCAAACCGCGGCGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAA 297
Db         10 AAGGTGCTCGTCGCCAATCGCGGGGAGATCGCGATCCGGGCCTTTCGTGCCGCCTACGAA 69

Qy        298 ACCGGTGCAGCCACGGTAGCTATTTACCCCCGTGAAGATCGGGGATCATTCCACCGCTCT 357
Db         70 CTGGGCGTCGGAACCGTGGCCGTTTATCCGTACGAGGACCGCAATTCGCAGCACCGTCTC 129

Qy        358 TTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGAC 417
Db        130 AAGGCGGACGAGTCTTACCAGATCGGCGACATCGGTCACCCGGTGCATGCATACCTGTCG 189

Qy        418 ATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATAC 477
Db        190 GTCGACGAGATCGTCGCGACGGCCCGTCGGGCGGGTGCCGACGCTATCTACCCTGGCTAC 249

Qy        478 GGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTACTTTT 537
Db        250 GGGTTTCTATCGGAGAATCCGGATCTGGCTGCGGCATGCGCGGCGGCGGGCATCAGCTTC 309

Qy        538 ATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAACCGCC 597
Db        310 GTCGGTCCCAGCGCCGAAGTGCTTGAGCTGGCTGGGAATAAGTCTCGCGCCATCGCGGCG 369

Qy        598 GCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAG 657
Db        370 GCCCGCGAAGCCGGCTTGCCCGTGCTGATGTCCTCGGCGCCGTCGGCCTCGGTCGACGAA 429

Qy        658 ATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGT 717
Db        430 CTGCTGTCGGTTGCGGCCGGCATGCCGTTTCCGTTGTTCGTCAAGGCAGTTGCCGGTGGC 489

Qy        718 GGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTAGCAACAGAA 777
Db        490 GGGGGCCGGGGTATGCGTCGTGTCGGCGATATCGCGGCGCTTCCGGAGGCGATCGAAGCC 549

Qy        778 GCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTG 837
Db        550 GCCAGCCGGGAAGCCGAGTCGGCGTTCGGGGACCCGACGGTCTATCTCGAGCAGGCAGTG 609

Qy        838 ATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACAC 897
Db        610 ATCAATCCACGCCACATCGAGGTGCAGATTCTGGCGGACAACCTCGGCGACGTGATCCAT 669

Qy        898 CTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCA 957
Db        670 CTCTATGAGCGTGACTGCAGTGTGCAGCGTCGCCATCAGAAGGTCATCGAGCTGGCGCCC 729

Qy        958 GCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGC 1017
Db        730 GCGCCGCACCTGGACGCCGAGTTGCGTTACAAGATGTGCGTCGATGCGGTCGCCTTCGCC 789

Qy       1018 CGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAAC 1077
Db        790 CGCCATATCGGGTACAGCTGCGCGGGCACCGTCGAGTTCCTGCTGGACGAGCGAGGGGAG 849

Qy       1078 CACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTC 1137
Db        850 TATGTCTTCATCGAGATGAATCCGCGGGTTCAGGTGGAGCACACGGTGACCGAGGAGATT 909

Qy       1138 ACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAA 1197
Db        910 ACCGACGTCGACCTGGTCGCCAGCCAGCTGCGCATTGCCGCCGGGGAGACGCTCGAACAA 969

Qy       1198 TTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACC 1257
Db        970 TTGGGCCTGCGGCAGGAGGACATCGCACCGCATGGCGCCGCACTACAGTGCCGGATCACC 1029

Qy       1258 ACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCA 1317
Db       1030 ACCGAGGATCCGGCCAACGGCTTCCGGCCGGACACGGGCCGGATCAGCGCGTTGCGCACC 1089

Qy       1318 CCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCA 1377
Db       1090 GCCGGCGGTGCCGGTGTCCGCCTGGACGGCAGCACCAACCTGGGCGCAGAAATCAGCCCG 1149

Qy       1378 CACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTT 1437
Db       1150 TACTTCGACTCCATGCTGGTCAAGCTGACCTGTCGGGGCCGTGACCTCCCTACCGCAGTG 1209

Qy       1438 GCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGT 1497
Db       1210 AGCCGTGCGCGCCGGGCGATCGCGGAGTTCCGGATCCGCGGGGTATCGACGAATATTCCG 1269

Qy       1498 TTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTC 1557
Db       1270 TTCCTGCAAGCGGTCCTGGATGACCCGGACTTCCGAGCGGGCCGGGTCACCACGTCCTTC 1329

Qy       1558 ATTGCCGATCACCCGCACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGGACGCATC 1617
Db       1330 ATTGATGAGCGGCCGCAGCTGCTGACCGCGCGCGCCTCGGCCGACCGCGGCACCAAGATC 1389

Qy       1618 CTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTT 1677
Db       1390 CTTAACTTCCTGGCCGATGTCACCGTCAACAACCCGTATGGCTCGCGTCCGTCAACGATC 1449

Qy       1678 GCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGT 1737
Db       1450 TACCCGGACGACAAGCTGCCCGATCTTGATCTGCGGGCCGCACCACCGGCCGGGTCCAAG 1509

Qy       1738 GACCGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCA 1797
Db       1510 CAGCGACTAGTCAAGTTGGGGCCGGAAGGATTTGCTCGTTGGCTGCGGGAGTCGGCCGCG 1569

Qy       1798 CTGGCAGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTC 1857
Db       1570 GTCGGGGTCACCGATACCACATTCCGGGATGCTCACCAGTCGTTACTGGCTACCCGAGTA 1629

Qy       1858 CGCTCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTG 1917
Db       1630 CGCACCAGCGGACTGTCGCGGGTGGCACCGTATCTCGCGCGGACCATGCCGCAGCTGTTG 1689

Qy       1918 TCCGTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGAT 1977
Db       1690 TCCGTGGAGTGTTGGGGCGGTGCGACTTACGATGTGGCGCTGCGCTTTCTCAAGGAGGAT 1749

Qy       1978 CCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTG 2037
Db       1750 CCCTGGGAACGGCTGGCCACACTGCGTGCAGCAATGCCCAATATCTGCTTGCAGATGCTA 1809

Qy       2038 CTTCGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTT 2097
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Db       1810 TTGCGGGGCCGCAATACCGTGGGCTACACGCCGTACCCGGAAATCGTGACGTCGGCGTTT 1869
Qy       2098 GTTAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGAC 2157
Db       1870 GTGCAAGAAGCAACAGCCACCGGTATCGACATCTTTCGTATCTTCGACGCGCTCAACAAC 1929
Qy       2158 GTCTCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAG 2217
Db       1930 ATCGAGTCGATGCGTCCGGCGATCGACGCAGTACGCGAAACAGGTTCTGCGATAGCAGAA 1989
Qy       2218 GTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGAT 2277
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Qy       2278 TACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAG 2337
Db       2050 TACTACCTGAAACTGGCTGAGCAGATCGTGGACGCCGGCGCCCATGTGCTGGCGATCAAG 2109
Qy       2338 GATATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCGCCGT 2397
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Qy       2398 GAATTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACC 2457
Db       2170 CGCTTCGACCTGCCCGTTCACCTGCACACCCACGACACACCGGGTGGCCAGCTCGCCAGC 2229
Qy       2458 TACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCT 2517
Db       2230 TATGTGGCCGCTTGGCACGCCGGGGCCGATGCCGTCGACGGCGCCGCCGCGCCGCTGGCG 2289
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Db       2290 GGAACGACCAGCCAGCCCGCGCTGAGCTCGATCGTTGCTGCCGCTGCCCACACCGAGTAC 2349
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Db       2350 GACACCGGCCTGTCGCTTTCGGCGGTGTGCGCCCTGGAGCCGTACTGGGAGGCGTTACGA 2409
Qy       2638 GGACTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCAC 2697
Db       2410 AAAGTGTATGCGCCGTTCGAGTCTGGGTTGCCGGGGCCGACGGGGCGGGTTTATCACCAC 2469
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Qy       2758 GATCGTTTCGAACTCATCGAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCA 2817
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Qy       2818 ACCAAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCG 2877
Db       2590 GTTAAGGTCACGCCAACGTCCAAGGTGGTCGGCGATCTGGCGCTGGCACTGGTCGGCGCC 2649
Qy       2878 GGTGTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCCAGACTCTGTC 2937
Db       2650 GGTGTCAGTGCAGACGAATTCGCCTCCGATCCAGCGCGATTTGGCATCCCGGAATCGGTA 2709
Qy       2938 ATCGCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAGCCACTGCGC 2997
Db       2710 CTCGGATTTCTGCGGGGCGAGCTGGGTGATCCGCCCGGCGGGTGGCCCGAACCGCTGCGC 2769
Qy       2998 ACCCGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAA 3057
Db       2770 ACTGCGGCGCTGGCCGGTCGCGGGGCGGCCAGGCCCACT---GCGCAATTGGCGGCGGAC 2826
Qy       3058 GAGCAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTG 3117
Db       2827 GACGAGATTGCCCTATCGTCGGTCGGAGCCAAG---CGTCAGGCCACCCTGAACAGGCTG 2883
Qy       3118 CTGTTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCT 3177
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Db       2884 TTATTTCCCAGTCCAACAAAGGAATTCAATGAGCACCGGGAAGCCTACGGCGACACGTCG 2943
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Qy       3238 CTGCCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAGCCAGACGAT 3297
Db       3004 CTG---GAGCGTGGGGTGGAGCTGTTGATCGGGCTGGAGGCCATTTCCGAACCCGACGAA 3060
Qy       3298 AAGGGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGT 3357
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Qy       3358 GACCGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCCAACAAGGGC 3417
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Qy       3418 CATGTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGTGATGAGGTC 3477
Db       3181 CACATCGCCGCGCCATTTGCCGGAGTCGTCACGGTCGGGGTGTGCGTCGGCGAGCGGGTC 3240
Qy       3478 AAGGCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCT 3537
Db       3241 GGCGCCGGCCAAACCATCGCCACCATCGAGGCGATGAAGATGGAAGCCCCGATCACCGCC 3300
Qy       3538 TCTGTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGGTGGC 3597
Db       3301 CCGGTTGCCGGCACCGTGGAGCGGGTGGCGGTGTCGGACACCGCCCAGGTGGAGGGCGGA 3360
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RESULT 9
US-10-282-122A-26500
; Sequence 26500, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

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;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26500
;   LENGTH: 3381
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis
US-10-282-122A-26500

  Query Match           35.7%;  Score 1292.2;  DB 12;  Length 3381;
  Best Local Similarity  62.0%;  Pred. No. 0;
  Matches 2095;  Conservative    0;  Mismatches 1273;  Indels    9;  Gaps    3;
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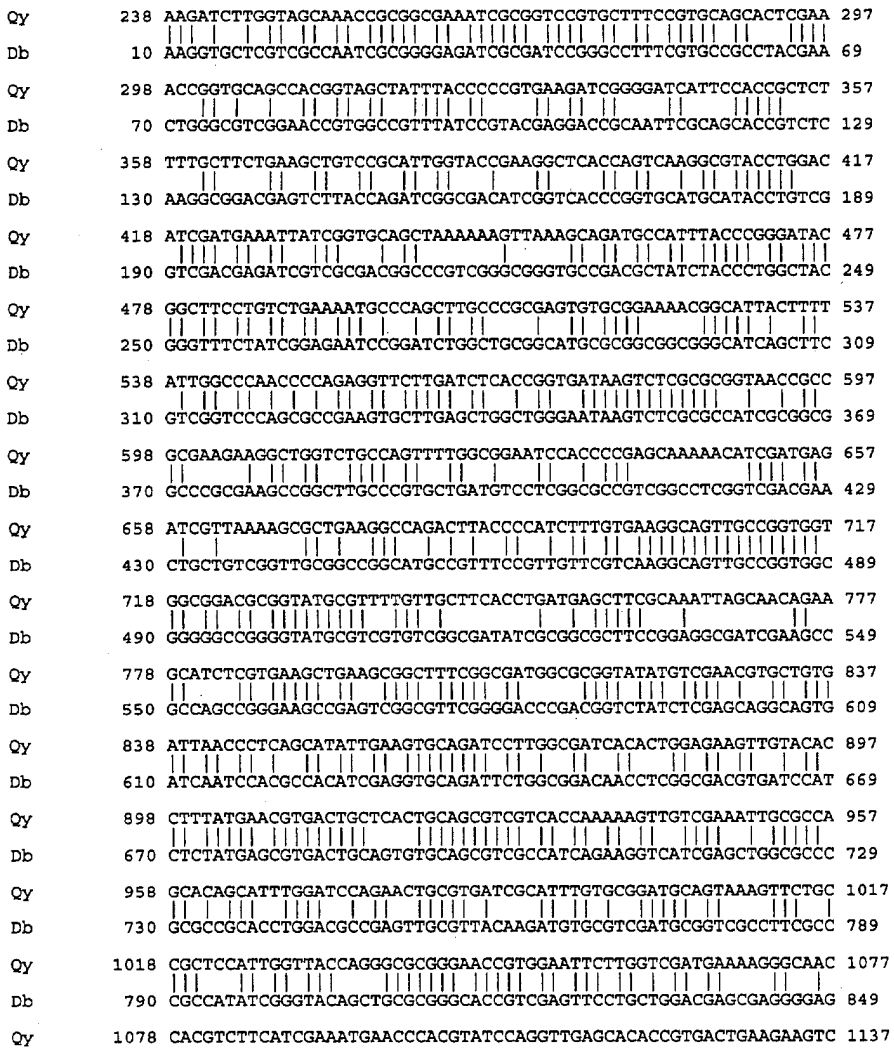

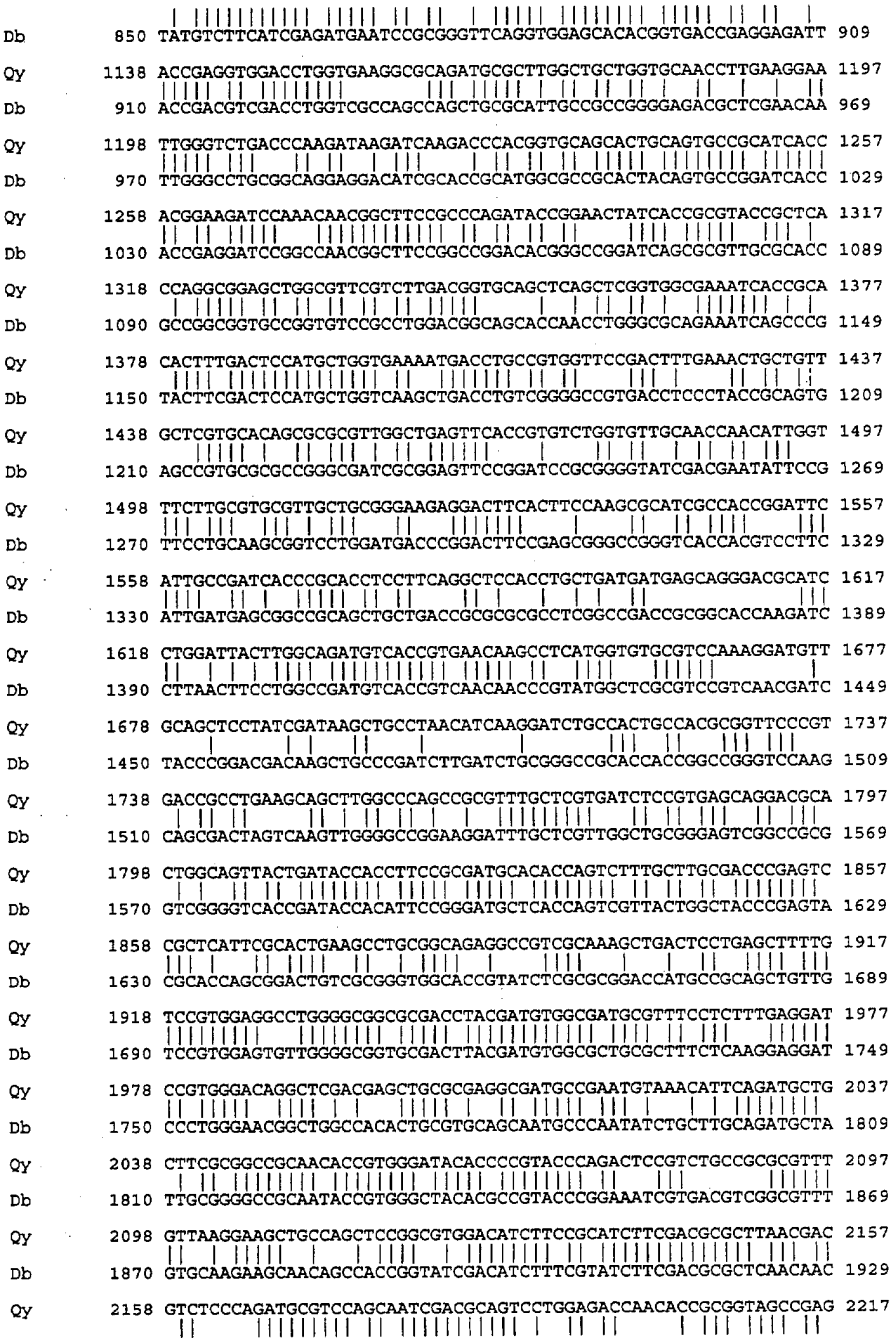

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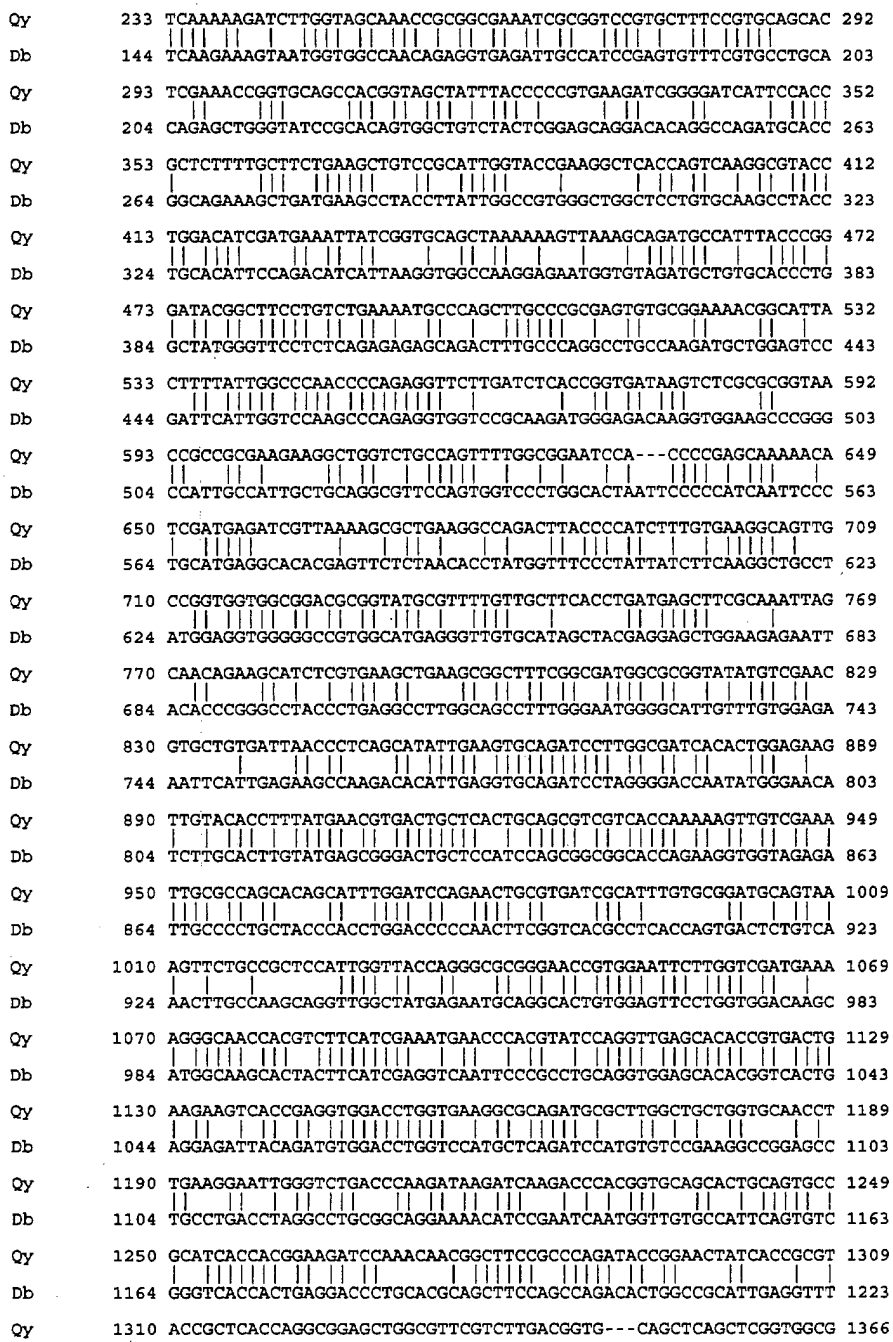
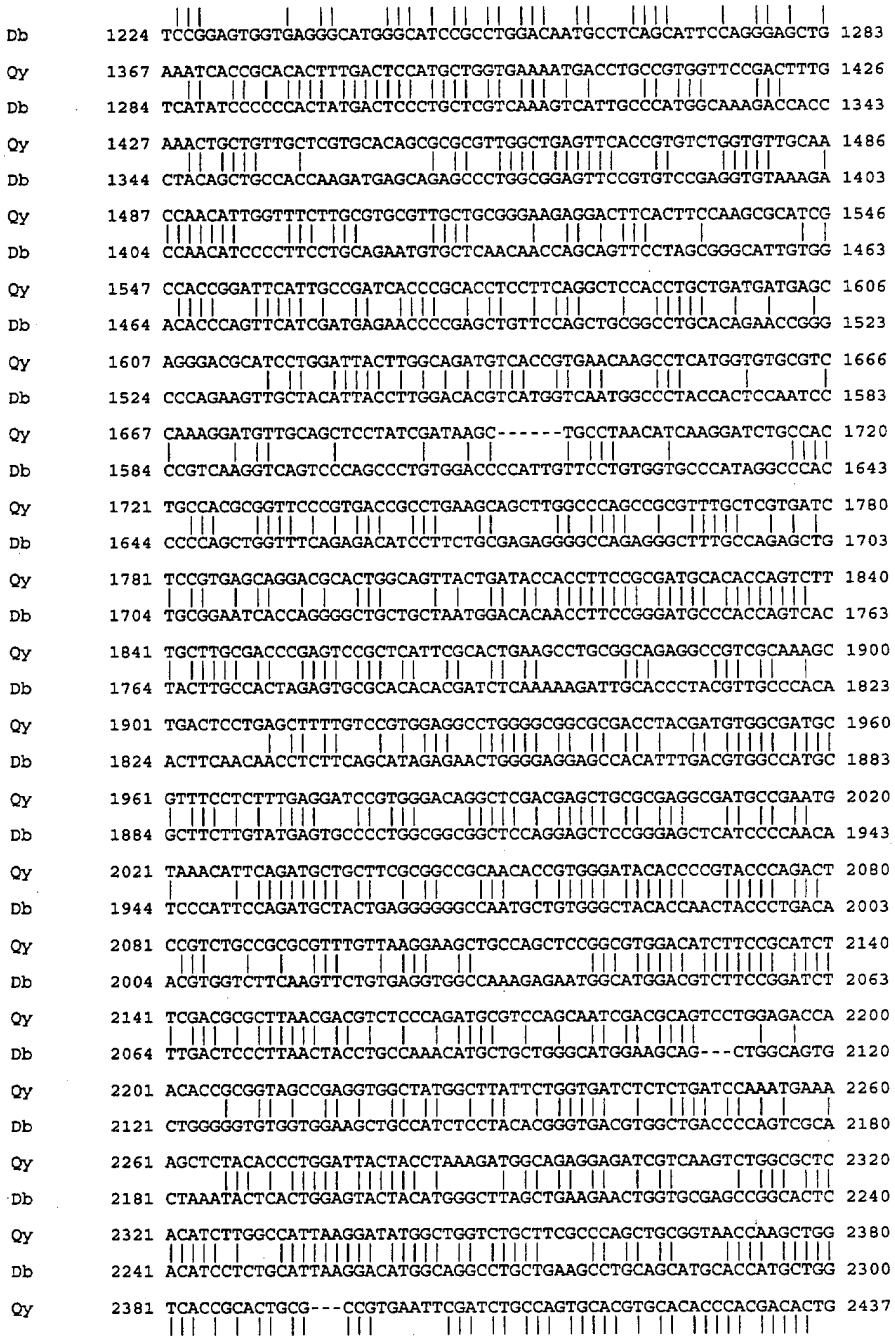
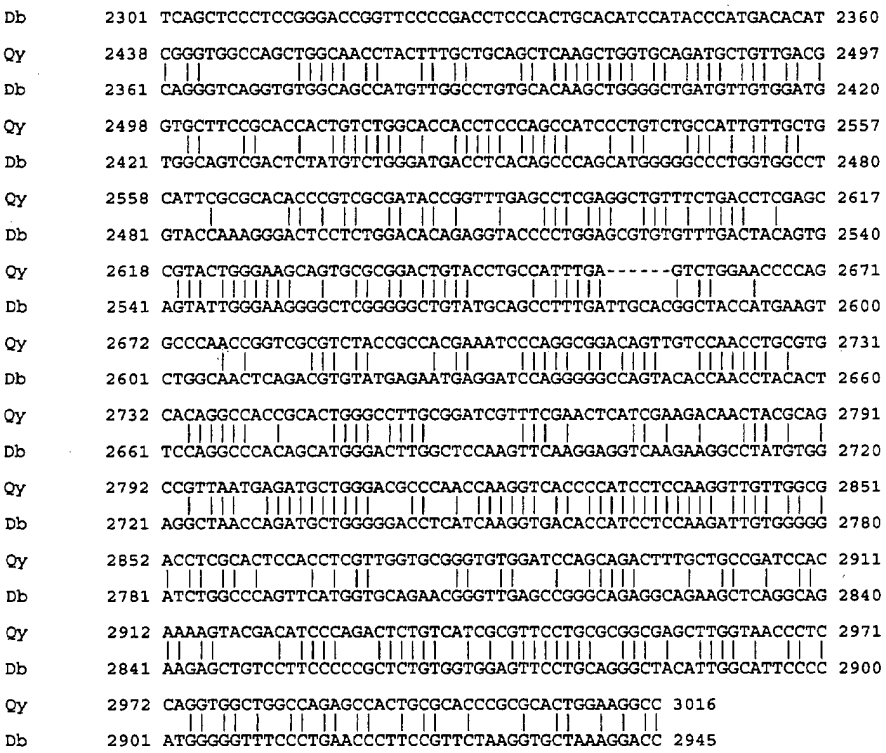
RESULT 10
US-09-917-800A-1566
; Sequence 1566, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1566
; LENGTH: 3945
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012744
US-09-917-800A-1566

Query Match 18.8%; Score 681; DB 9; Length 3945;
Best Local Similarity 54.2%; Pred. No. 3.2e-197;
Matches 1521; Conservative 0; Mismatches 1260; Indels 24; Gaps 6;







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RESULT 11
US-09-880-107-3029
; Sequence 3029, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3029
;   LENGTH: 4017
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 S72370
US-09-880-107-3029

  Query Match             18.7%;  Score 677.4;  DB 9;  Length 4017;
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  Matches 1525;  Conservative    0;  Mismatches 1256;  Indels   24;  Gaps    7;
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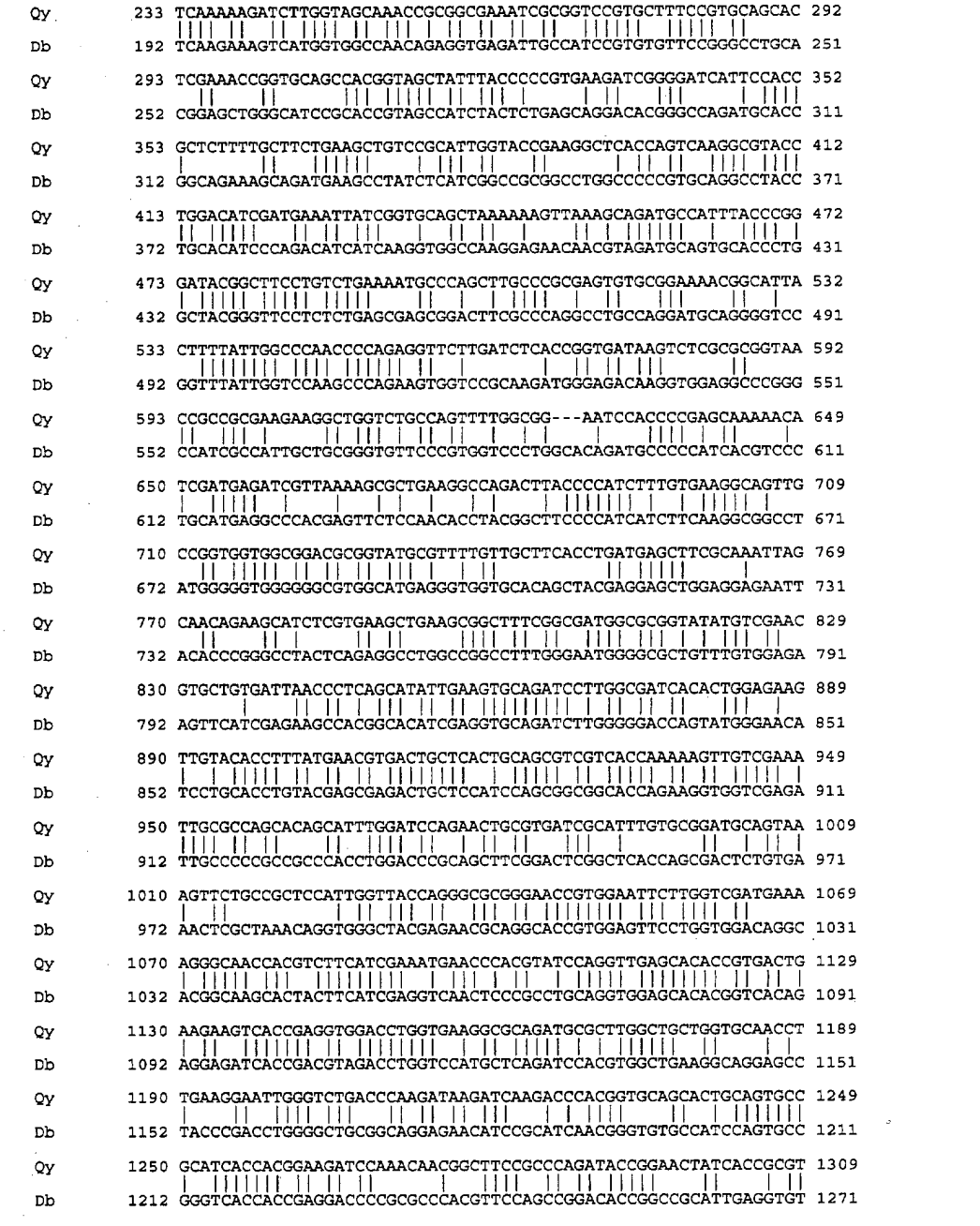
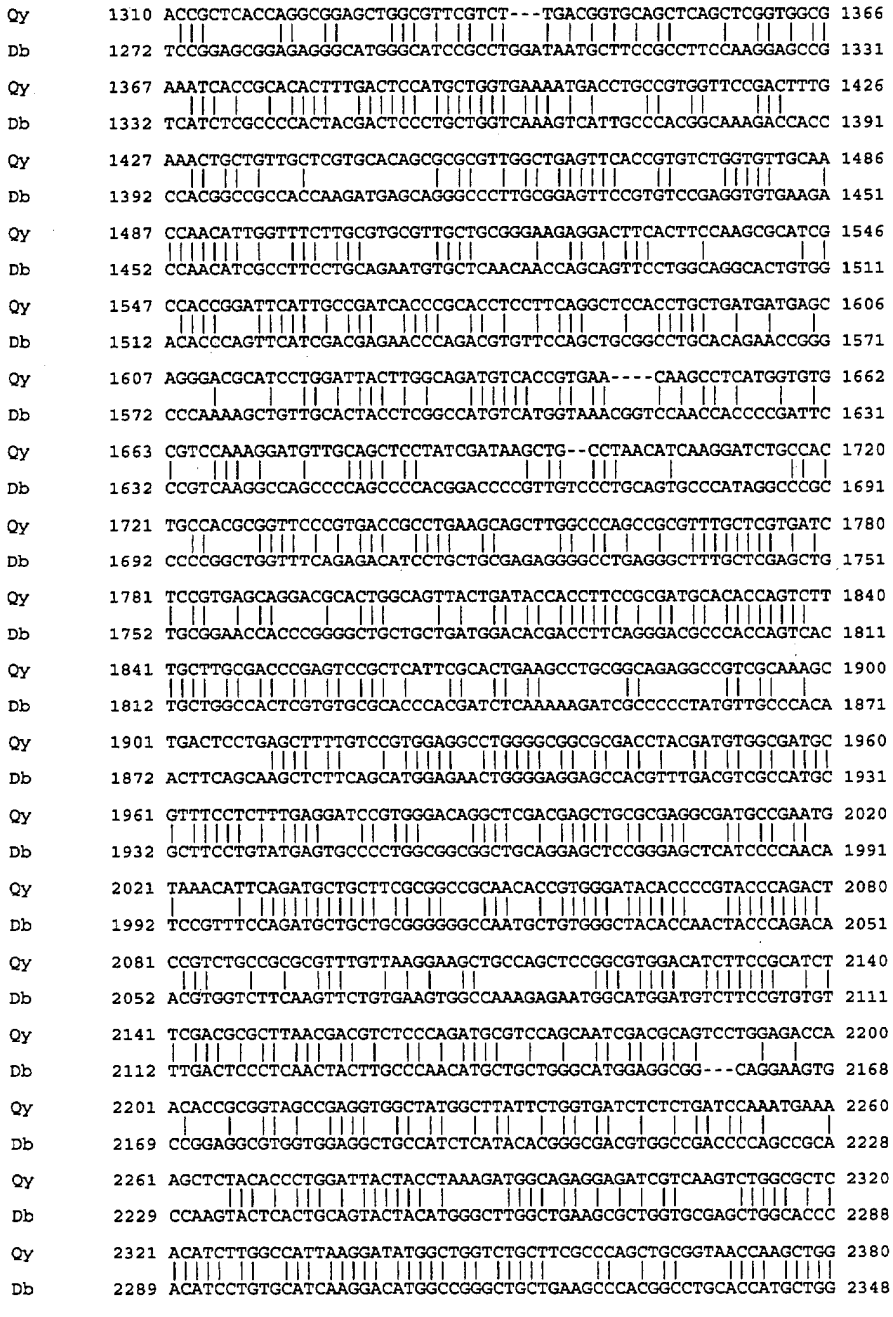
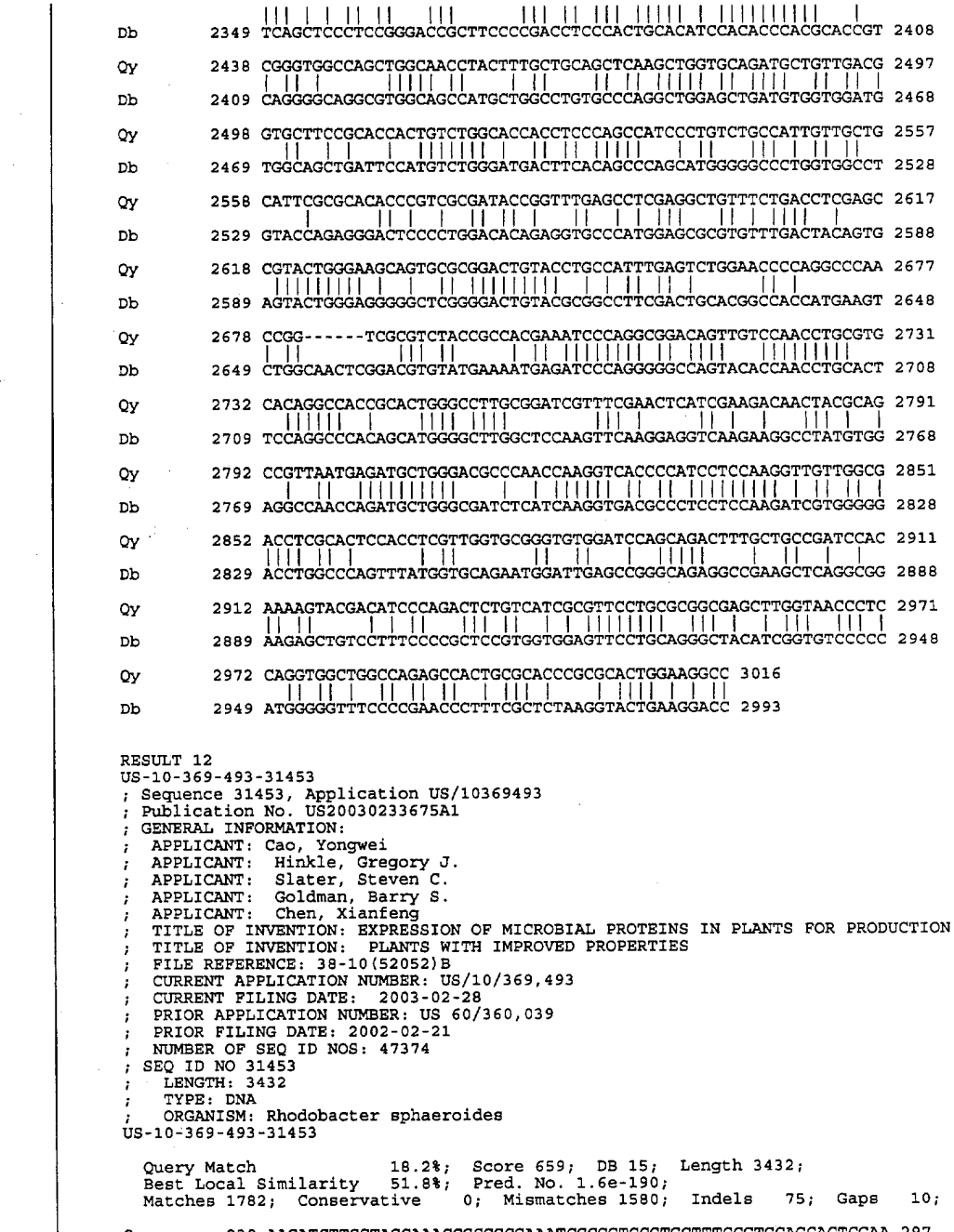
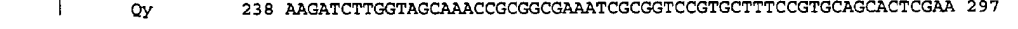


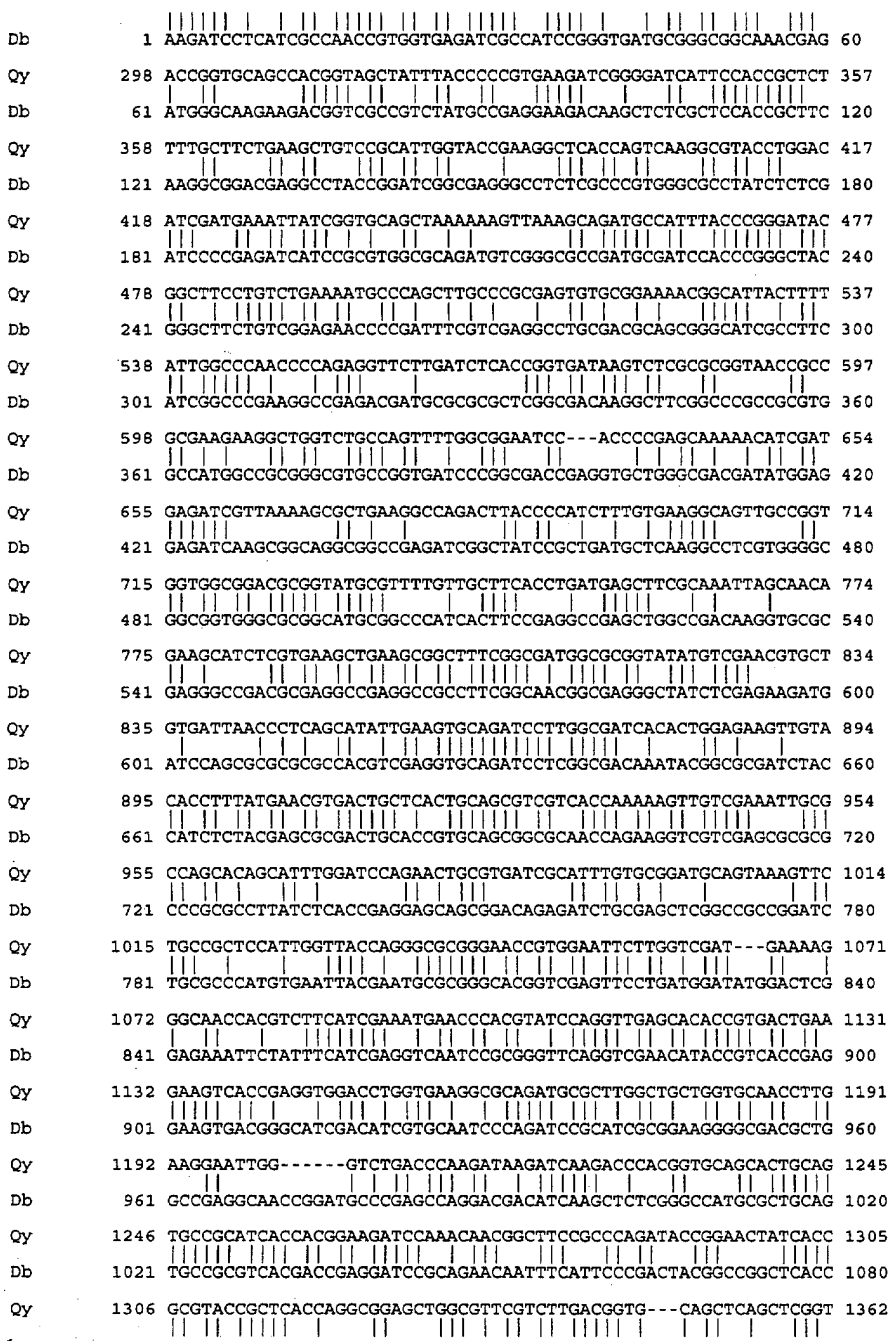


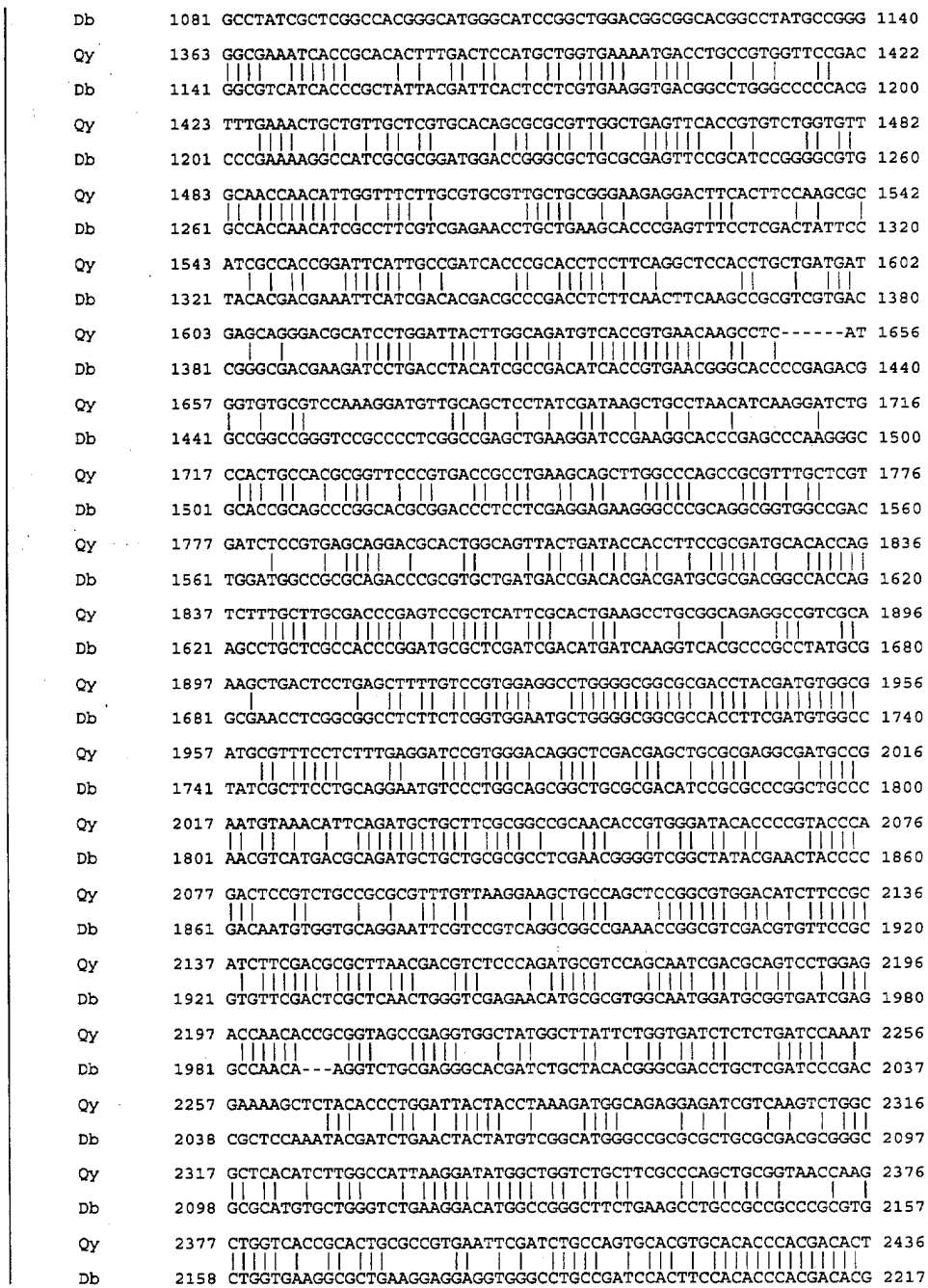


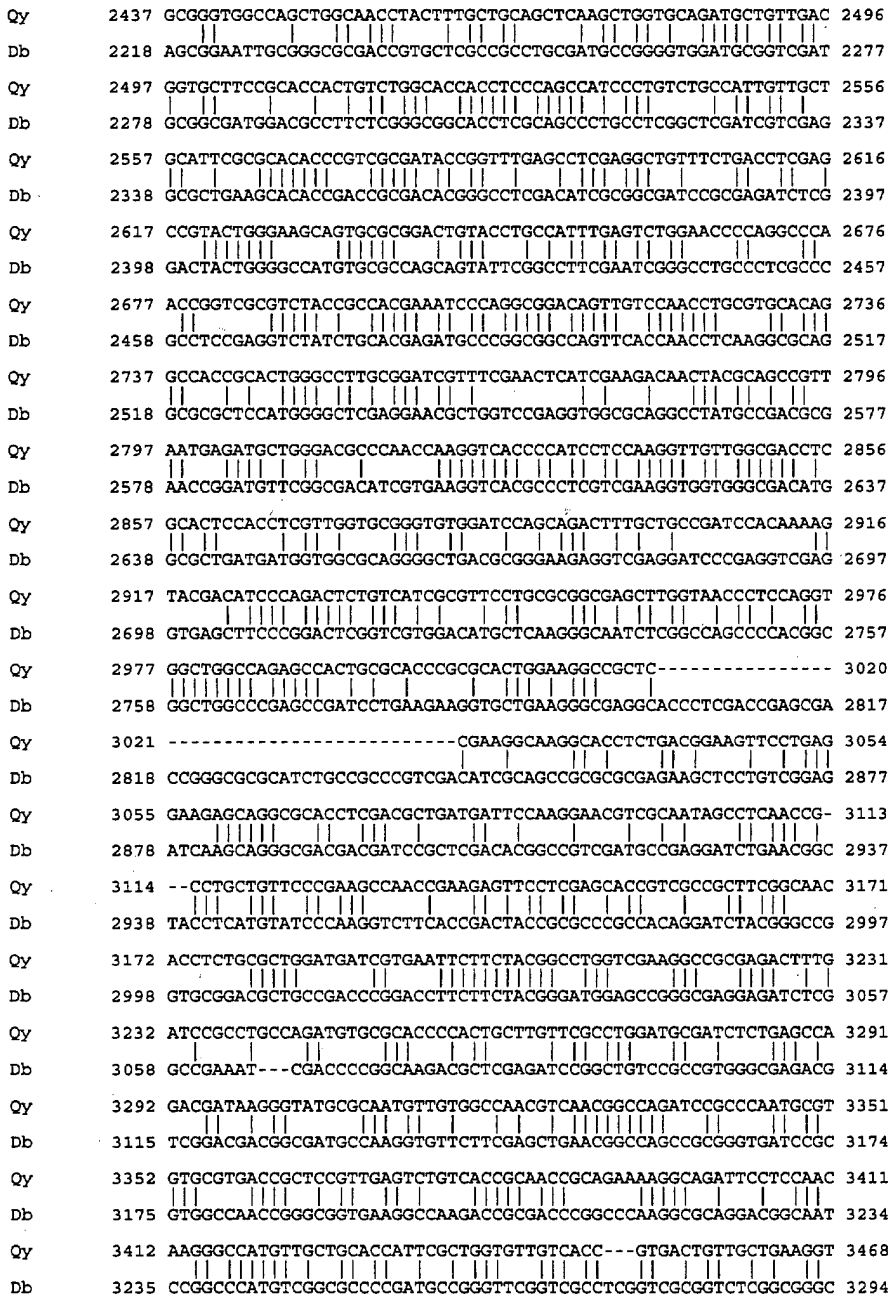
RESULT 12
US-10-369-493-31453
; Sequence 31453, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 31453
; LENGTH: 3432
; TYPE: DNA
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-31453

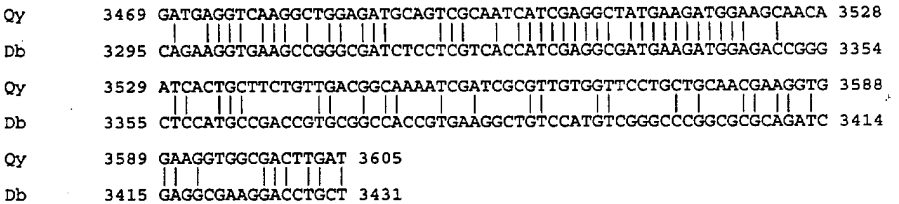
Query Match 18.2%; Score 659; DB 15; Length 3432;
Best Local Similarity 51.8%; Pred. No. 1.6e-190;
Matches 1782; Conservative 0; Mismatches 1580; Indels 75; Gaps 10;





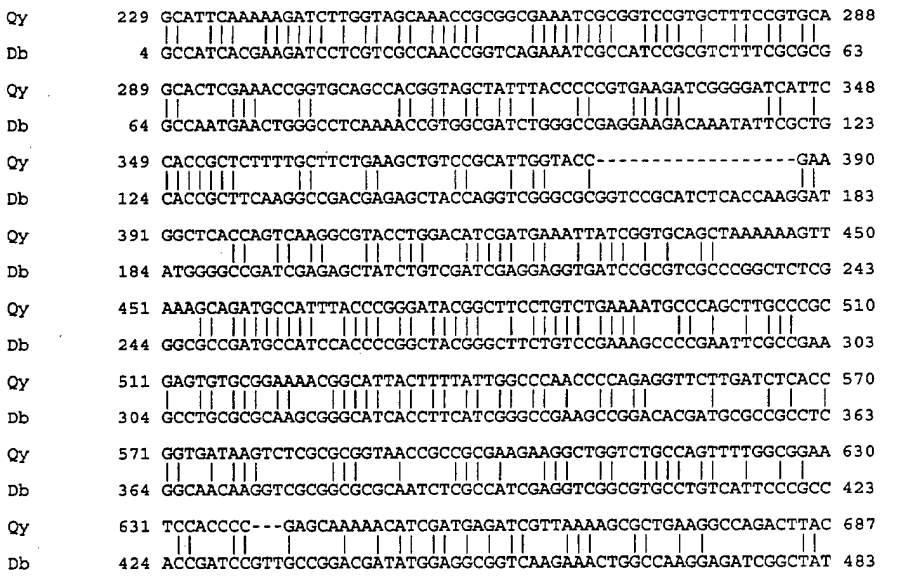


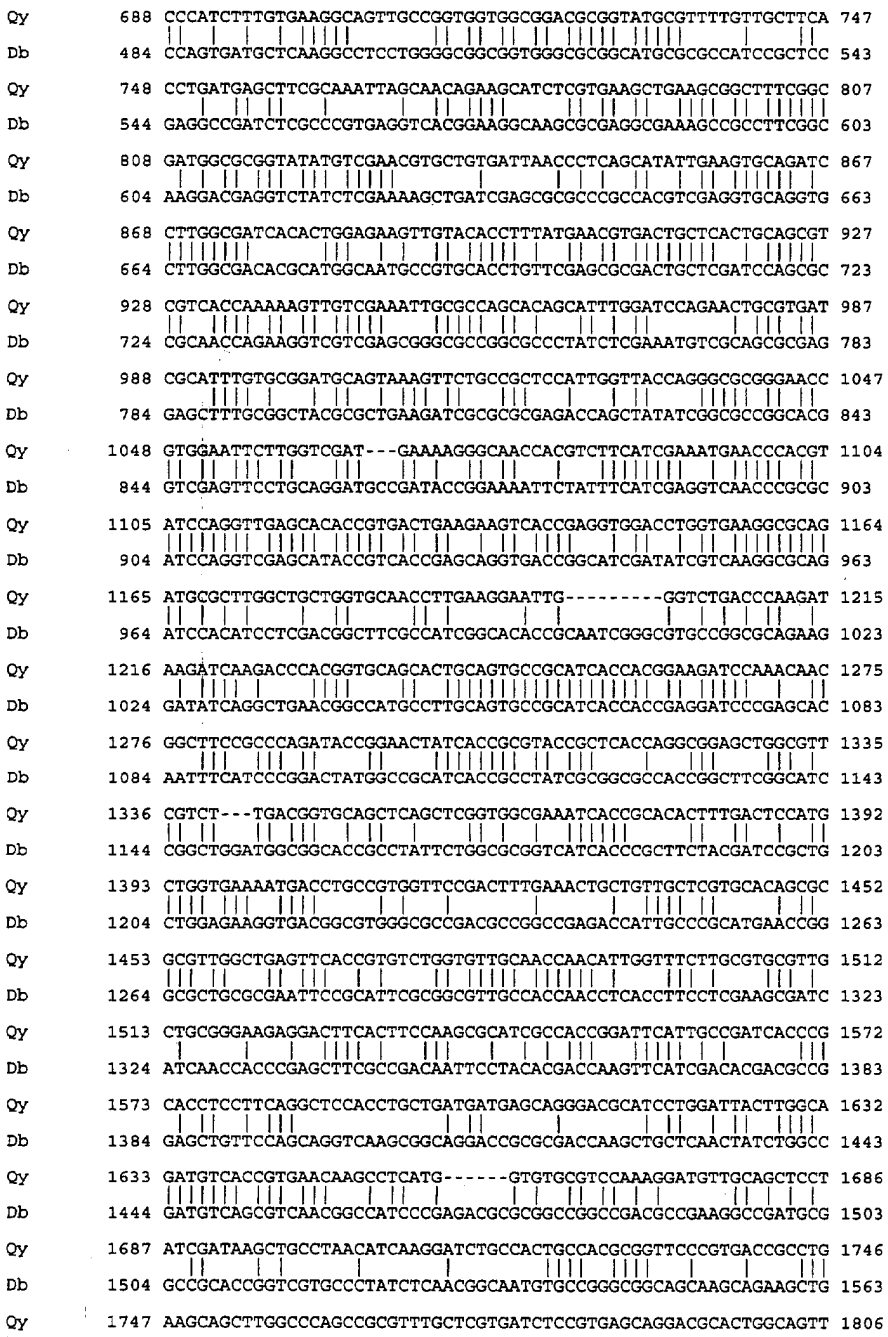


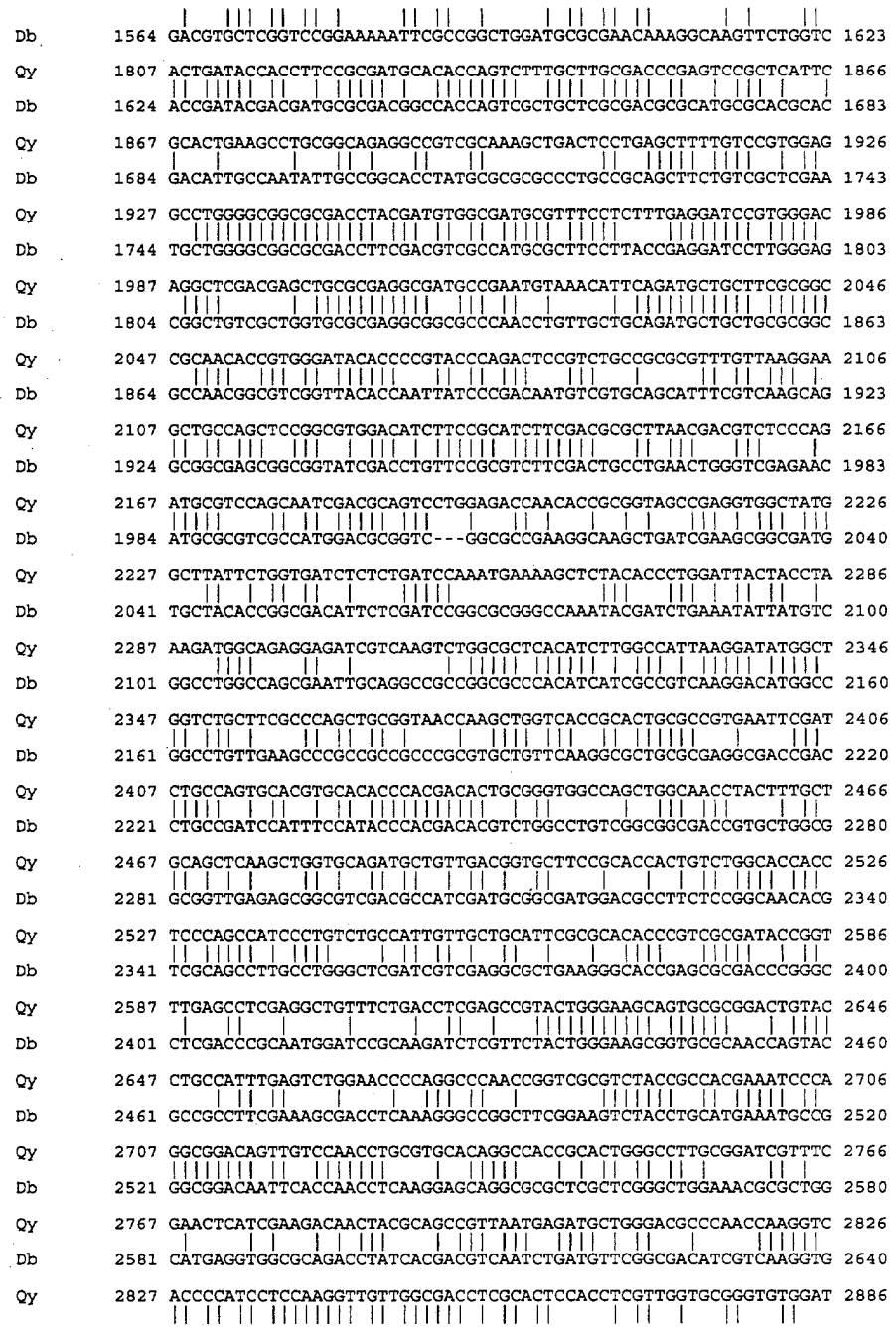


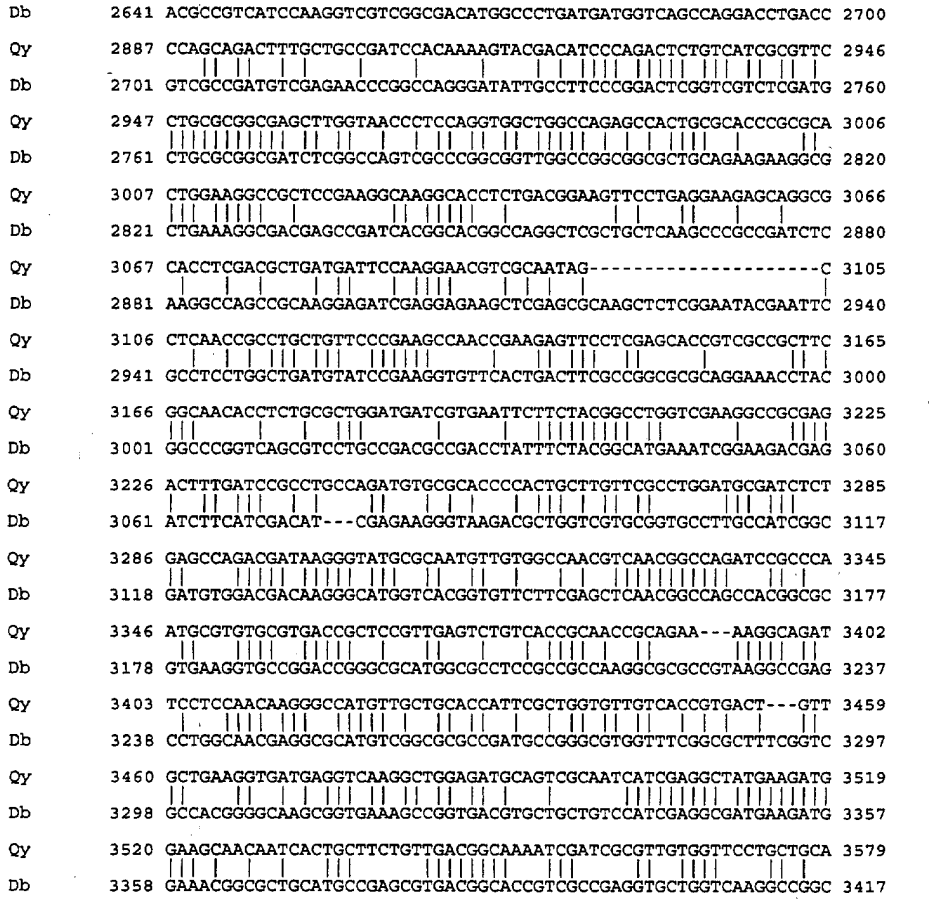
RESULT 13
US-10-369-493-35714
; Sequence 35714, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35714
; LENGTH: 3459
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35714

Query Match 17.8%; Score 643.6; DB 15; Length 3459;
Best Local Similarity 51.6%; Pred. No. 8.7e-186;
Matches 1788; Conservative 0; Mismatches 1599; Indels 75; Gaps 11;









RESULT 14
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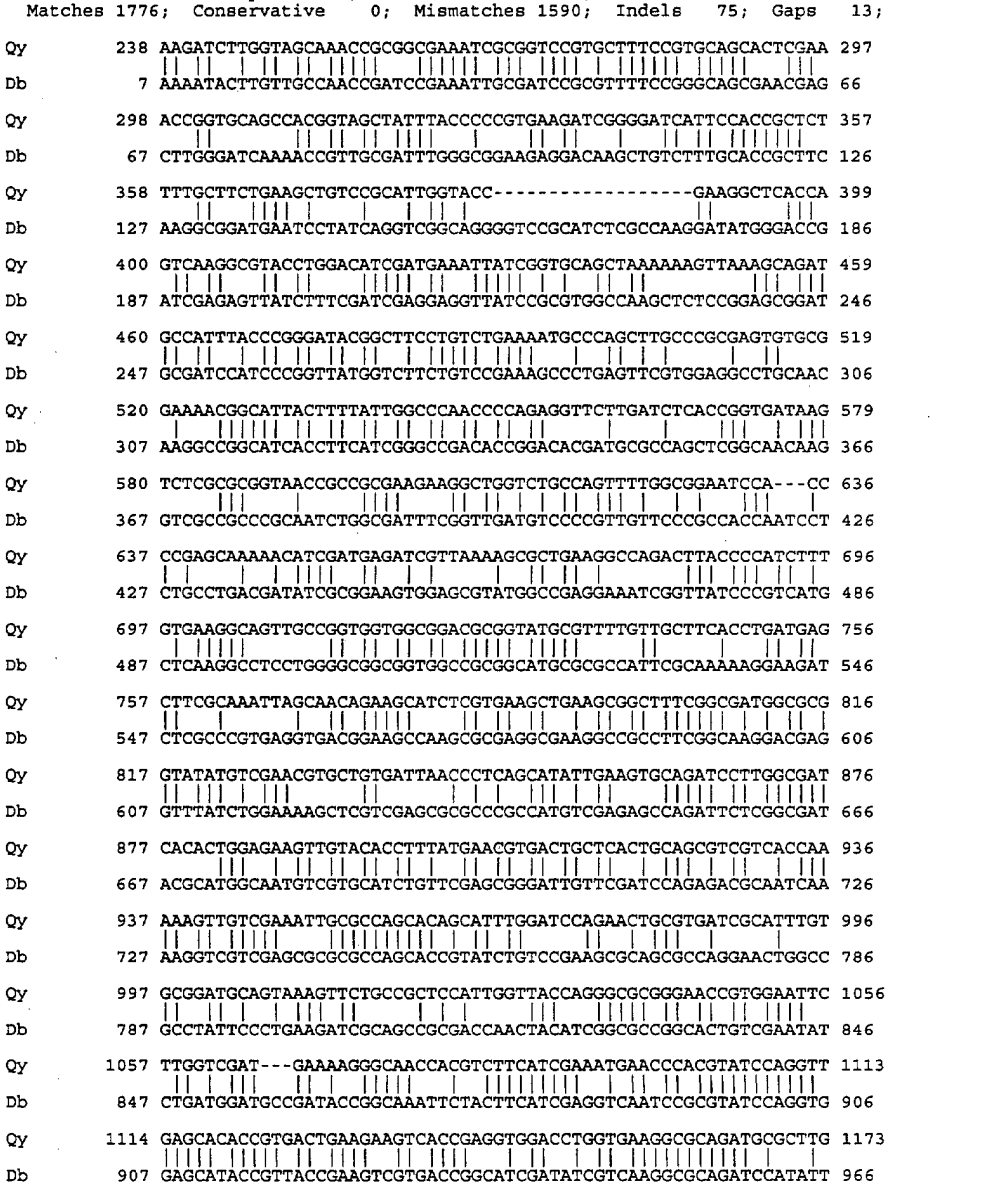
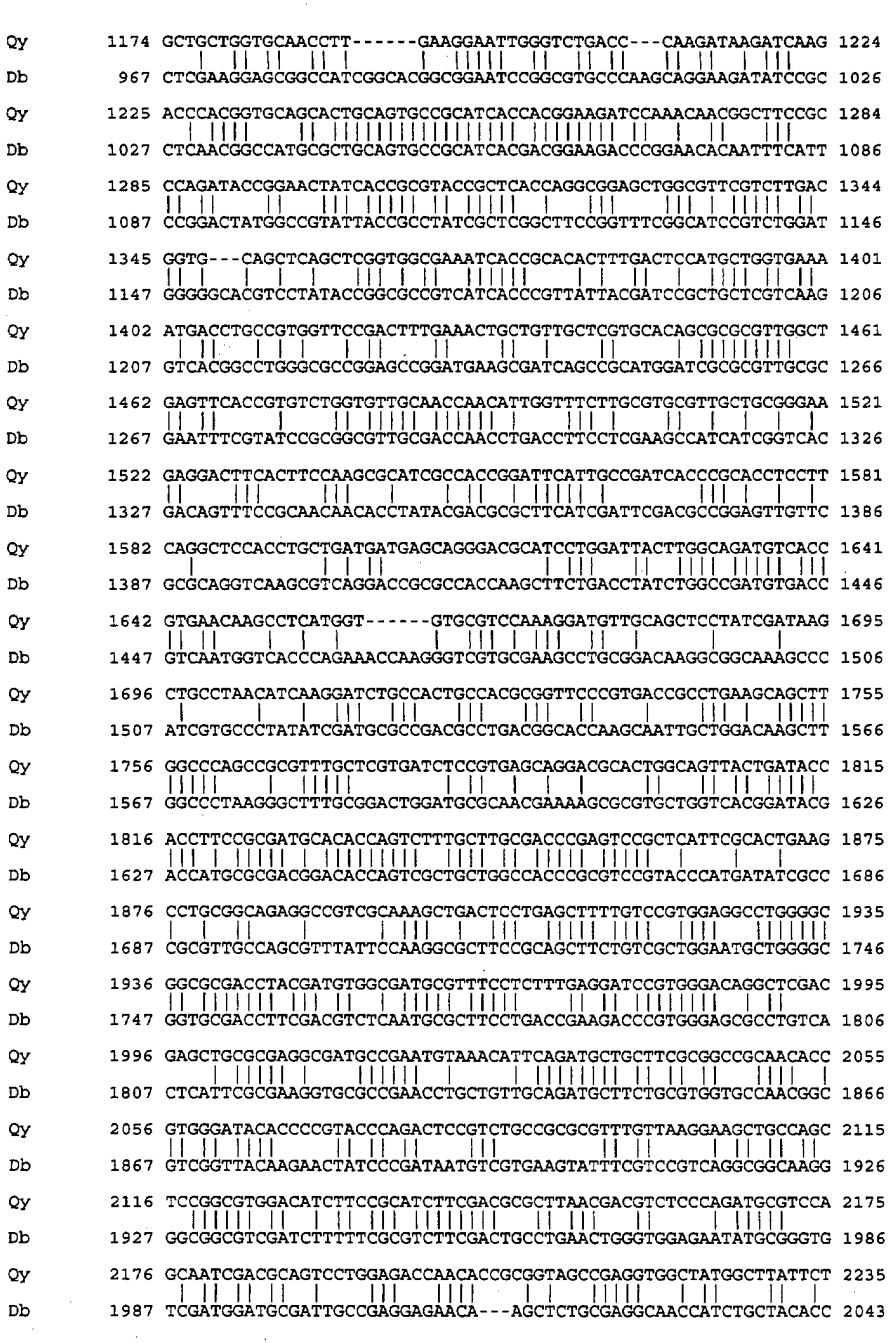
; Sequence 35137, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 35137
; LENGTH: 3441
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-35137

Query Match 17.0%; Score 617; DB 15; Length 3441;
Best Local Similarity 51.6%; Pred. No. 1.2e-177;
Matches 1776; Conservative 0; Mismatches 1590; Indels 75; Gaps 13;

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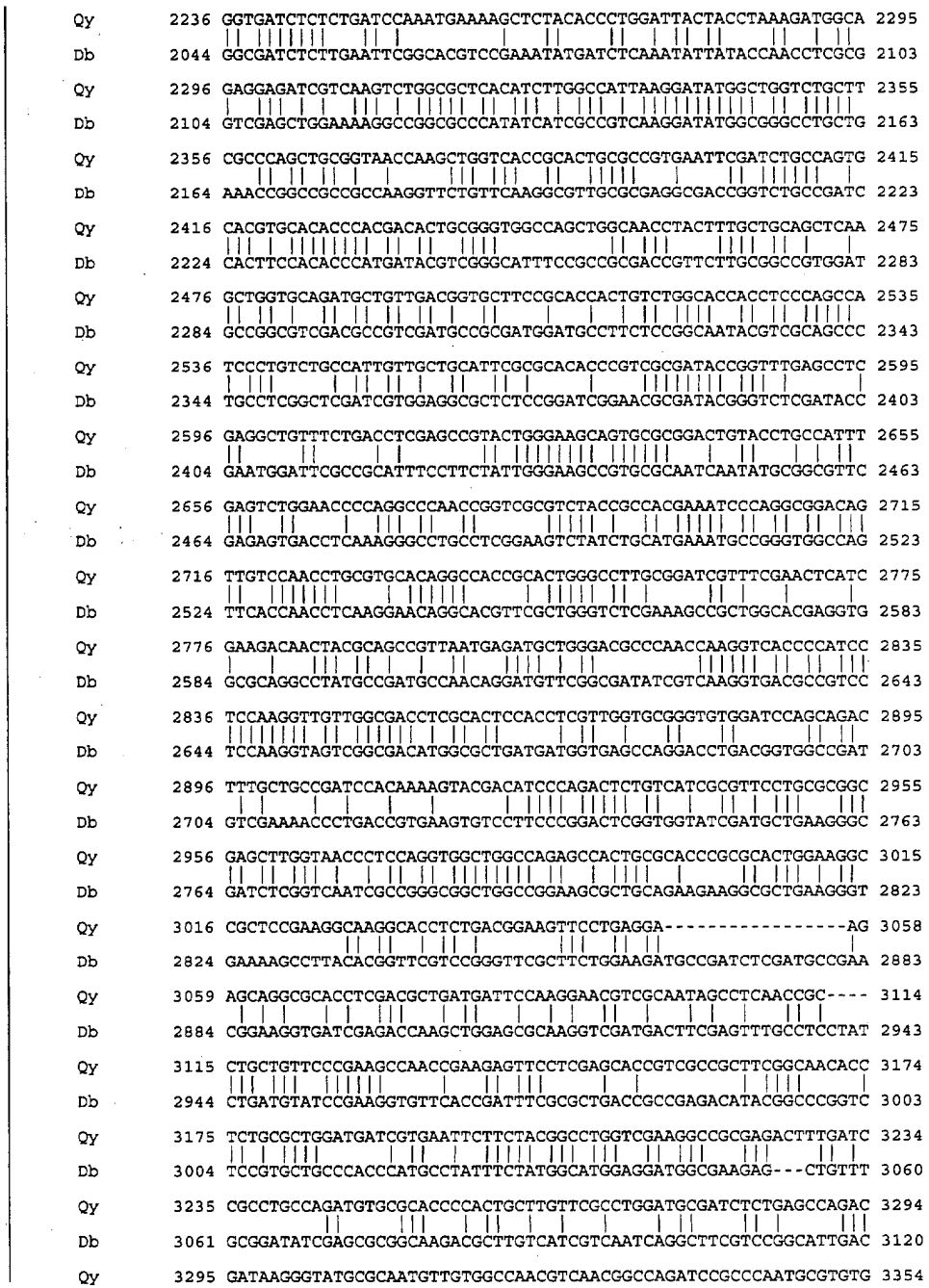
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Qy 2656 GAGTCTGGAACCCCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAG 2715
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Db 2524 TTCACCAACCTCAAGGAACAGGCACGTTCGCTGGGTCTCGAAAGCCGCTGGCACGAGGTG 2583
Qy 2776 GAAGACAACTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCC 2835
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Qy 3175 TCTGCGCTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACTTTGATC 3234
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Qy       3469 GATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACA 3528

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; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38504
;   LENGTH: 3453
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38504

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  Matches 1776;  Conservative    0;  Mismatches 1590;  Indels   75;  Gaps   13;

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Db         73 CTTGGGATCAAAACCGTTGCGATTTGGGCGGAAGAGGACAAGCTGTCTTTGCACCGCTTC 132

Qy        358 TTTGCTTCTGAAGCTGTCCGCATTGGTACC----------------GAAGGCTCACCA 399

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Qy        400 GTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAAGTTAAAGCAGAT 459

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Qy        460 GCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCG 519

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Qy        520 GAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAG 579

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Qy        580 TCTCGCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCA---CC 636

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Qy        937 AAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGT 996

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Qy       1174 GCTGCTGGTGCAACCTT------GAAGGAATTGGGTCTGACC---CAAGATAAGATCAAG 1224

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Qy       1462 GAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAA 1521

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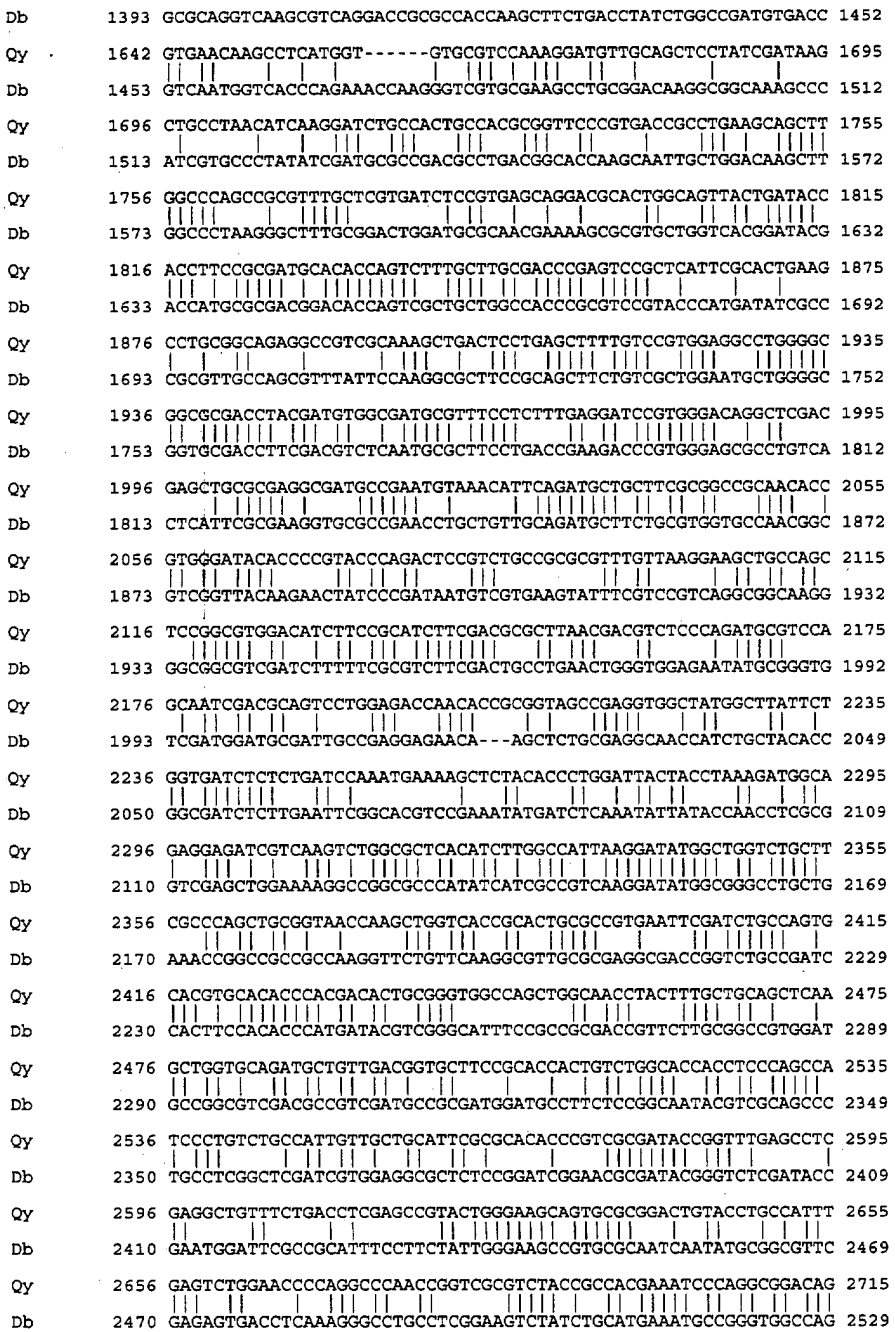

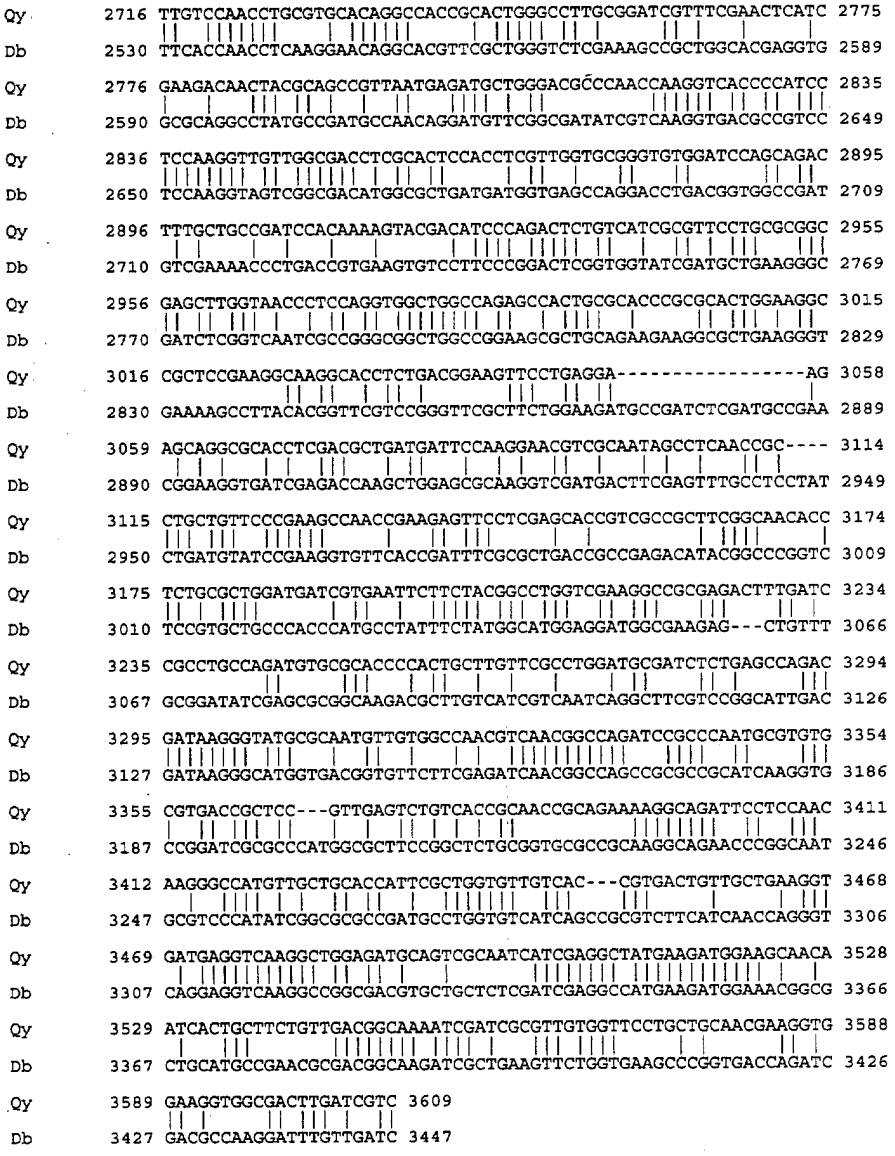

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Job time : 1227 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 18:35:49 ; Search time 8670 Seconds
(without alignments)
12471.852 Million cell updates/sec

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Perfect score: 3621
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	609.8	16.8	3537	29	AY408287	AY408287 Mus muscu
	2	606.2	16.7	3537	29	AY408285	AY408285 Homo sapi
	3	442.4	12.2	3537	29	AY408286	AY408286 Pan trogl
	4	432.2	11.9	2877	11	AK077665	AK077665 Mus muscu
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	6	236	6.5	903	13	BQ881271	BQ881271 AGENCOURT
c	7	223.4	6.2	859	28	AQ875053	AQ875053 V120F6 mT
	8	220.2	6.1	637	10	BF251052	BF251052 EST418309
	9	216.6	6.0	862	14	CA793824	CA793824 AGENCOURT
	10	216.4	6.0	675	9	AI109467	AI109467 GH08678.5
	11	214.8	5.9	744	12	BI103175	BI103175 602889415
	12	213.2	5.9	800	14	CK000115	CK000115 AGENCOURT
	13	211	5.8	640	12	BI618593	BI618593 RH49459.5
	14	208.2	5.7	715	12	BG910468	BG910468 602806142
	15	204.4	5.6	641	12	BJ063722	BJ063722 BJ063722
	16	202.8	5.6	635	14	CB576991	CB576991 AMGNNUC:C
	17	202.8	5.6	696	12	BP177875	BP177875 BP177875
c	18	200.6	5.5	516	28	BZ293357	BZ293357 CG0285.r1
	19	200.6	5.5	758	14	CF869970	CF869970 tric021xb
	20	200.6	5.5	813	14	CB900127	CB900127 tric021xb
	21	199	5.5	887	10	BF781506	BF781506 602104410
	22	198.4	5.5	546	14	CB279857	CB279857 ru88d01.y
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	24	195.6	5.4	508	12	BI621845	BI621845 RH53265.5
	25	193.6	5.3	666	12	BI605019	BI605019 RH70532.5
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	28	191	5.3	625	9	AI293242	AI293242 GH16378.5
	29	190.6	5.3	611	10	BE312170	BE312170 601152484
	30	189.2	5.2	915	13	BQ730755	BQ730755 AGENCOURT
	31	188.4	5.2	1030	29	CNS06M6L	AL405091 T3 end of
	32	188.2	5.2	949	13	BQ752438	BQ752438 EST633001
	33	188	5.2	921	13	BQ959497	BQ959497 AGENCOURT
	34	187.4	5.2	599	10	BF506511	BF506511 AT09003.5
	35	185.2	5.1	910	14	CD244370	CD244370 AGENCOURT
	36	185	5.1	923	13	BQ734080	BQ734080 AGENCOURT
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	41	183.6	5.1	556	9	AI134619	AI134619 GH12134.5
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	43	182.4	5.0	725	12	BG599744	BG599744 EST504639
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ALIGNMENTS

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LOCUS AY408287 3537 bp DNA linear GSS 15-DEC-2003
DEFINITION Mus musculus PC gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY408287
VERSION AY408287.1 GI:39764258
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3537)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3537)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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ORIGIN

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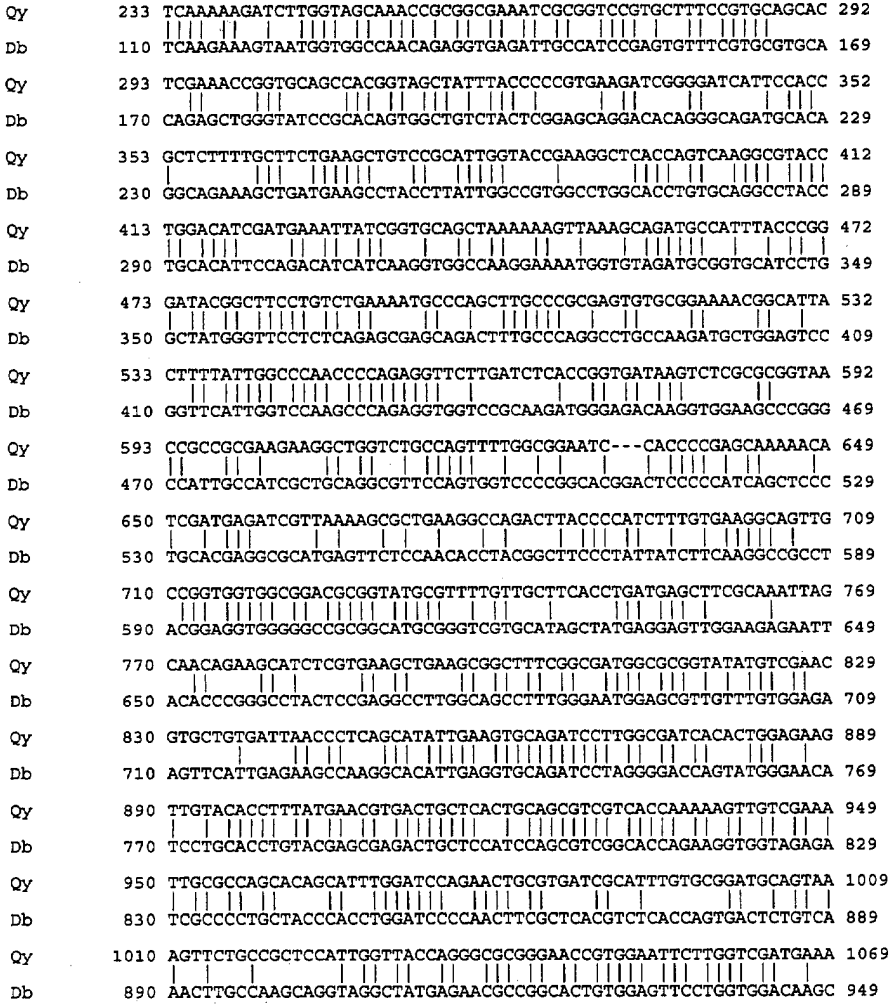
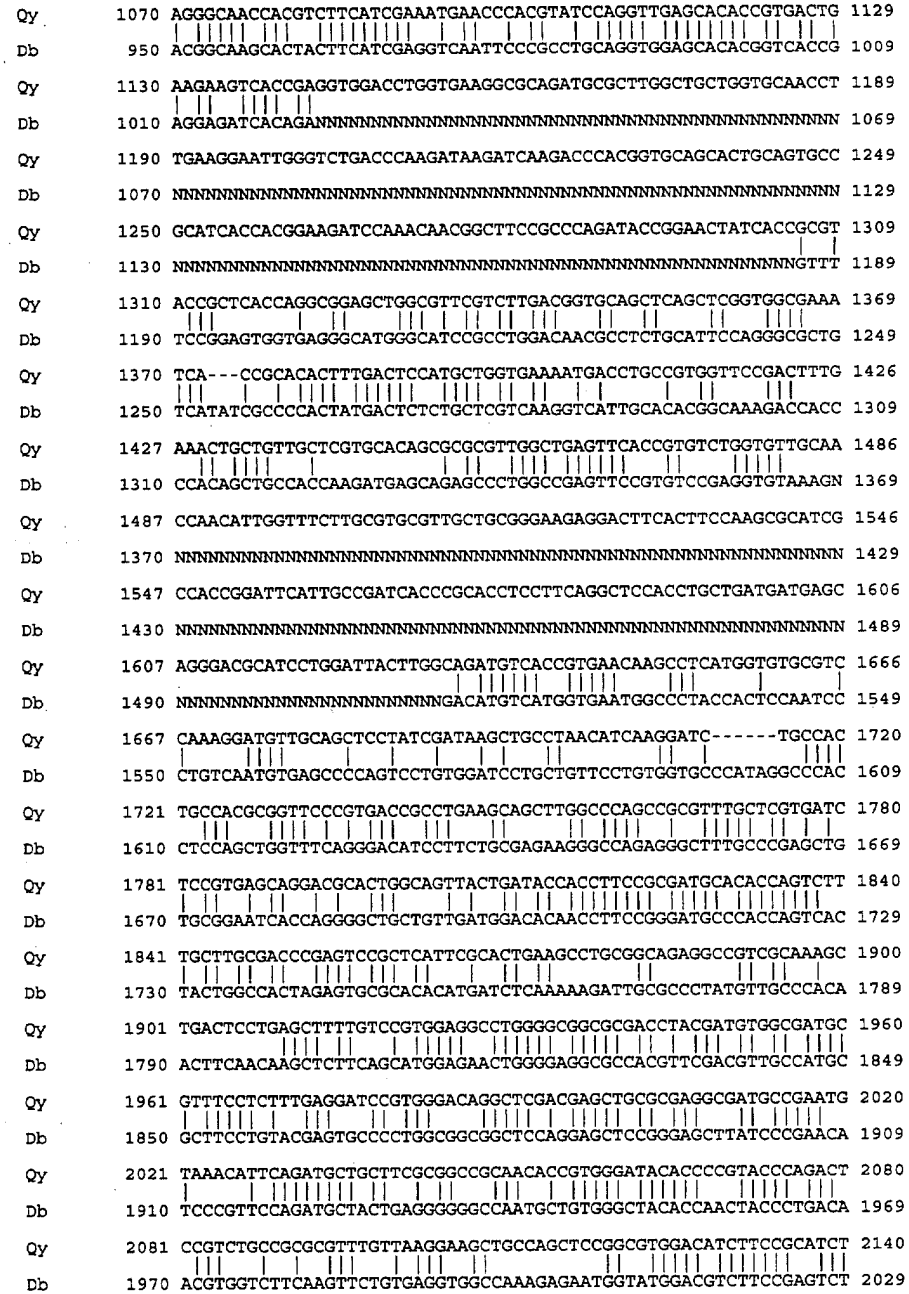
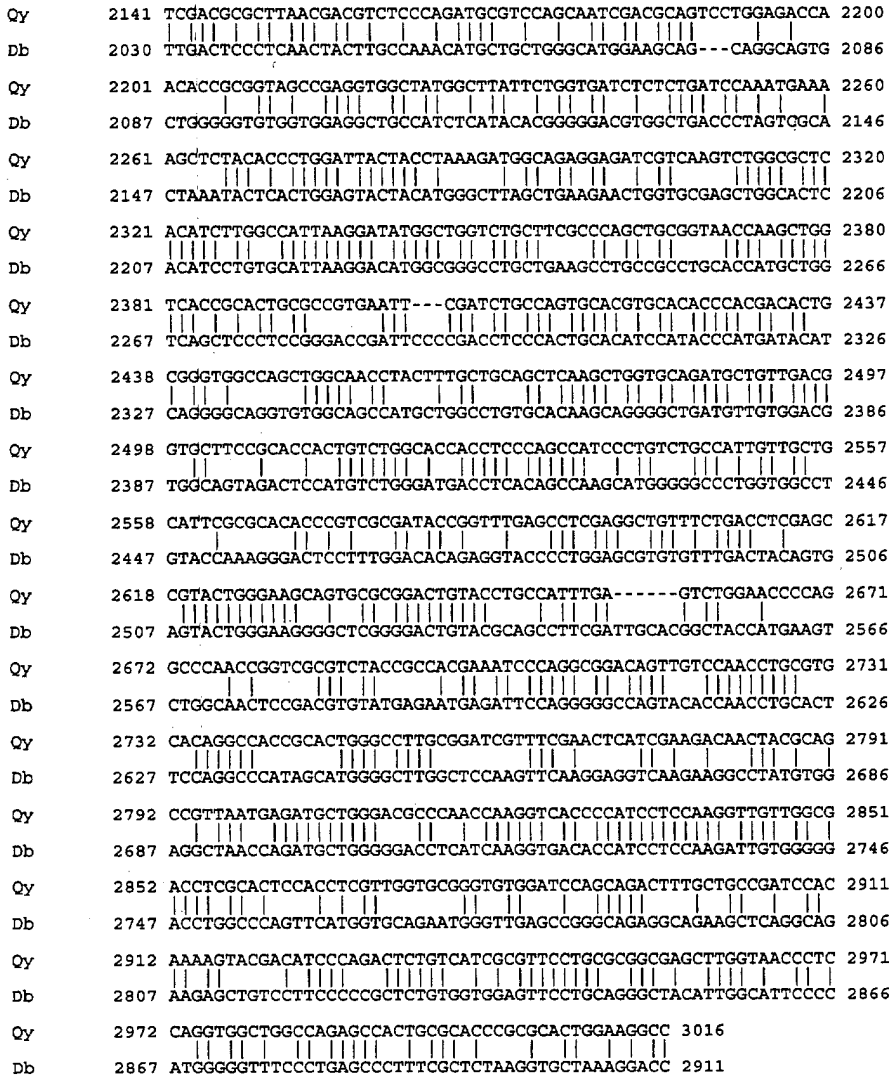
Best Local Similarity 48.5%; Pred. No. 2.2e-131;
Matches 1361; Conservative 0; Mismatches 1420; Indels 24; Gaps 6;







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DEFINITION Homo sapiens PC gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY408285
VERSION AY408285.1 GI:39764256
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3537)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3537)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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ORIGIN

Query Match 16.7%; Score 606.2; DB 29; Length 3537;
Best Local Similarity 48.7%; Pred. No. 1.5e-130;
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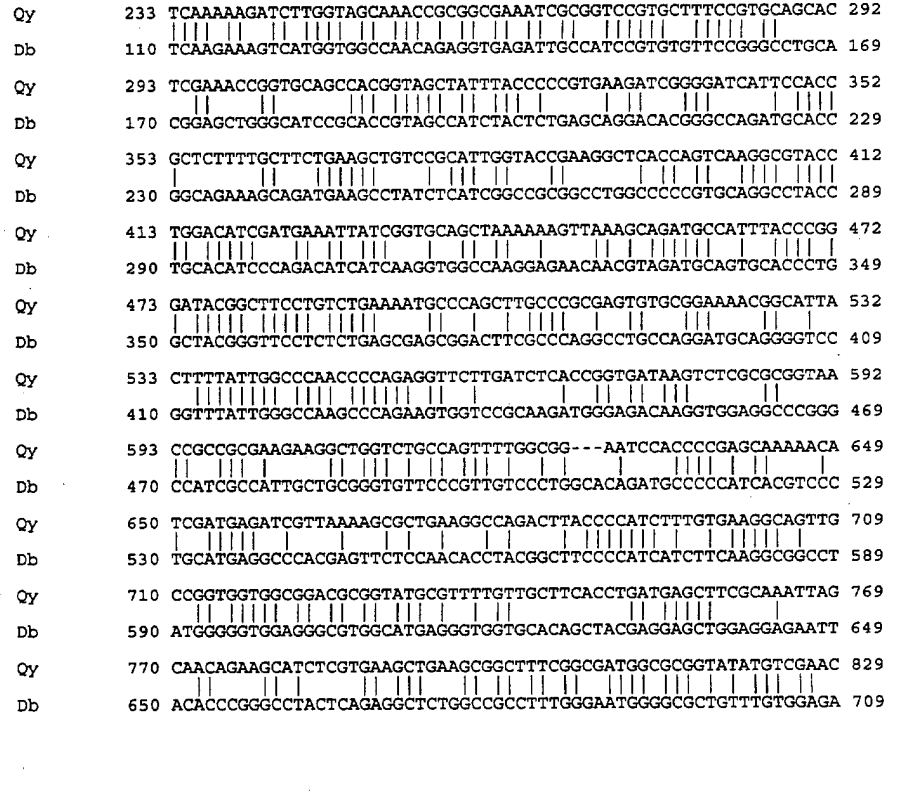

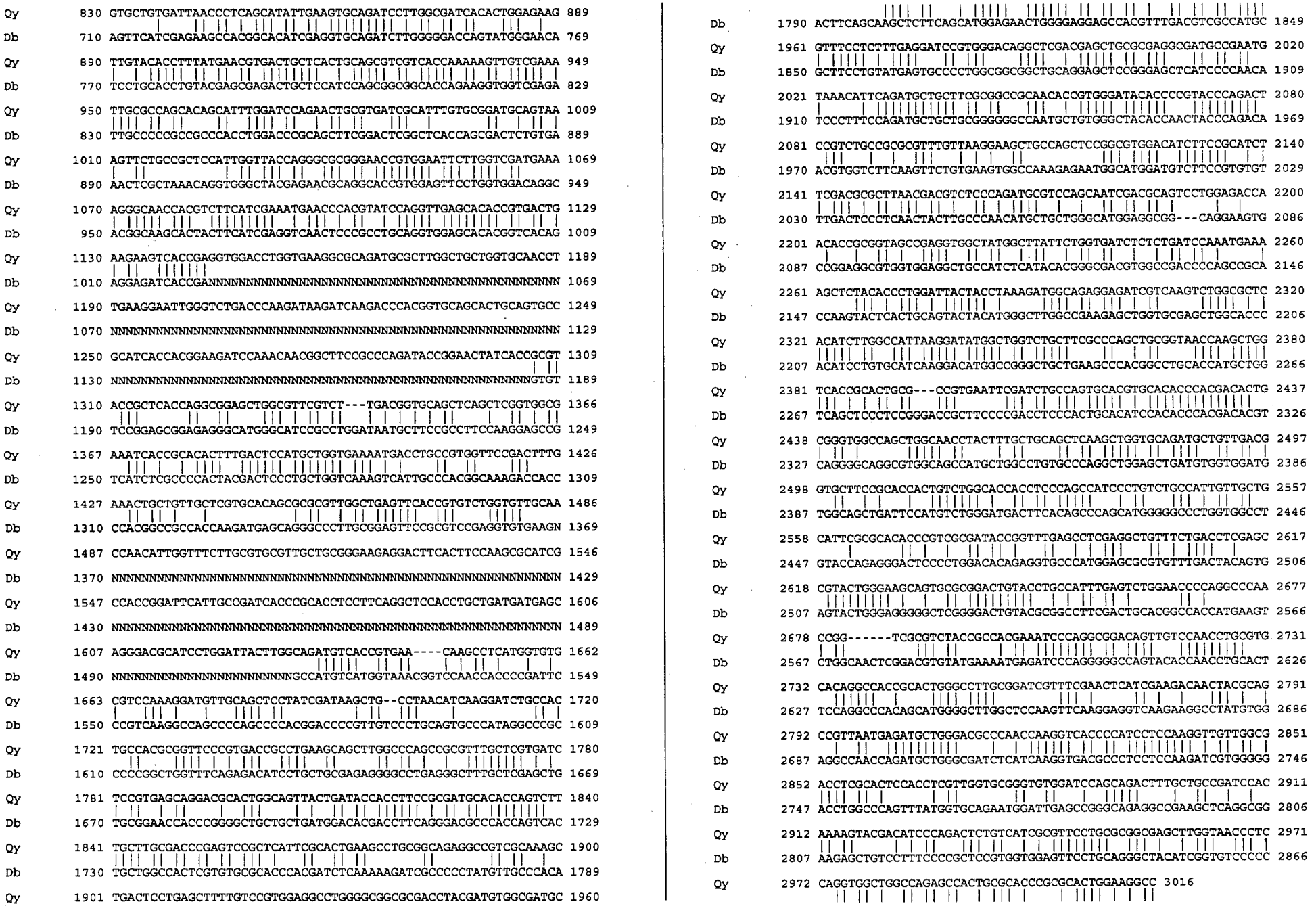

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RESULT 3
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LOCUS       AY408286               3537 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Pan troglodytes PC gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY408286
VERSION     AY408286.1  GI:39764257
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 3537)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3537)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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ORIGIN

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Db        290 TGCACATCCCAGACATCATCAAGGTGGCCAAGGAGAACAACGTAGATGCAGTACACCCTG 349

Qy        473 GATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGCATTA 532
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Qy        593 CCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGG---AATCCACCCCGAGCAAAAACA 649

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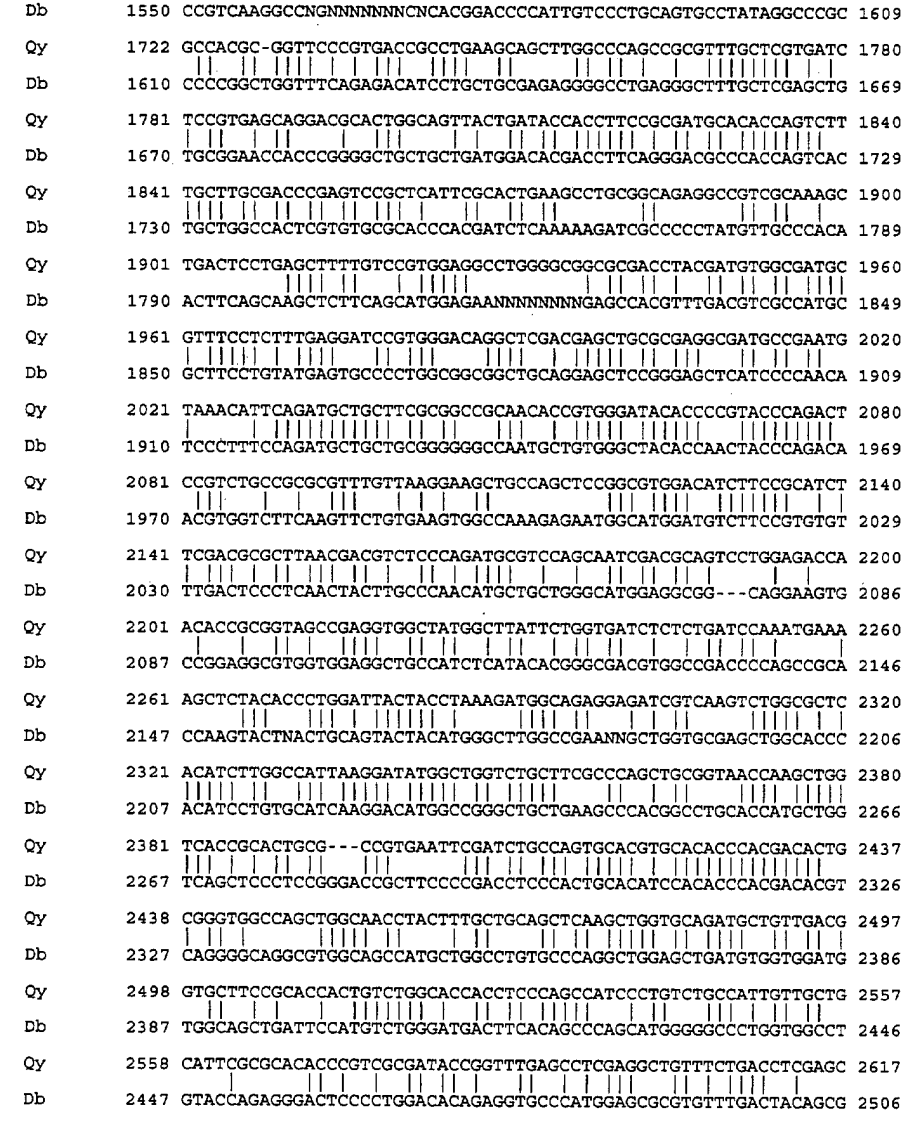

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DEFINITION Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730513C12 product:pyruvate decarboxylase, full insert sequence.

ACCESSION AK077665
VERSION AK077665.1 GI:26346580
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2877)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/

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Qy       2832 ATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCGGGTGTGGATCCAGC 2891

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REFERENCE   1  (bases 1 to 888)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
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            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 888)
  AUTHORS   Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
            Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
            Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 11.
            Kluyveromyces lactis
  JOURNAL   FEBS Lett. 487 (1), 66-70 (2000)
  MEDLINE   20584721
   PUBMED   11152886
REFERENCE   3  (bases 1 to 888)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     This GSS is part of a random genomic sequencing program of thirteen
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            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
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            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var.  hansenii, Pichia sorbitophila,
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ORIGIN
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Qy        455 CAGATGCCATTTACCCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGT 514

Db        795 TGAACTTTATCCATCCTGGTTACGGGTTCCTATCAGAAAACTCTGAATTCGCTGAAAAAG 736

Qy        515 GTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTG 574

Db        735 TTGCAGCTTCTGGTATCACTTGGGTTGGTCCTCCAGCTGCTGTTATCGATTCCGTTGGTG 676

Qy        575 ATAAGTCTCGCGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCA 634

Db        675 ACAAAGTTTCAGCCAGAAACTTGGCTGAAAAGGCTAACGTTCCAGTGGTTCCAGGTACTC 616

Qy        635 C---CCCGAGCAAAAACATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCA 691

Db        615 CAGGTCCAATTGAGACTGTCGAAGAAGCACAGGCCTTCGTTGATAAATACGGATTCCCAG 556

Qy        692 TCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTG 751

Db        555 TCATCATTAAGGCCGCCTTTGGTGGTGGTGGTCGTGGTATGAGAGTTGTCCGTGAAGGTG 496

Qy        752 ATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATG 811

Db        495 ATGATATCAGTGACGCTTTCCAACGTGCCAAATCTGAAGCTATCACTGCTTTTGGTAACG 436

Qy        812 GCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTG 871

Db        435 GTACTTGTTTCATTGAAAGATTCTTGGACAAGCCAAAGCATATCGAAGTTCAATTGTTGG 376

Qy        872 GCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTC 931

Db        375 CTGATAACTACGGTAACGTTGTTCATCTGTTCGAAAGAGATTGTTCCGTTCAAAGAAGAC 316

Qy        932 ACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCA 991

Db        315 ATCAAAAGGTTGTCGAAGTTGCCCCAGCCAAAACTCTACCTGAAGAAGTGCGTGACGCTA 256

Qy        992 TTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGG 1051

Db        255 TCTTAACTGATGCGGTCAAATTAGCTAAGGAAGCTGGTTACAGAAACGCTGGTACCGCTG 196

Qy       1052 AATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGG 1111

Db        195 AATTCTTAGTCGATAACCAAAACAGACATTACTTTATCGAAATTAACCCAAGAATTCAAG 136
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Qy       1112 TTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCT 1171
Db        135 TCGAACATACAATTACCGAAGAAATCACCGGTATCGATATCGTCGCTGCTCAAATCCAAA 76

Qy       1172 TGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACG 1231
Db          75 TCGCTGCAGGTGCCACTTTGGAACAATTGGGTTTGATGCAAGATAAGATTACAACTCGTG 16

Qy       1232 GTGCAGCACTGCAGT 1246
Db          15 GTTTCGCCATCCAGT 1
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RESULT 6
BQ881271

LOCUS	BQ881271 903 bp mRNA linear EST 16-AUG-2002
DEFINITION	AGENCOURT_7978339 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6185002 5', mRNA sequence.
ACCESSION	BQ881271
VERSION	BQ881271.1 GI:22273279
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 903)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. James R. Lupski cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13575 row: b column: 11 High quality sequence stop: 692.

FEATURES	Location/Qualifiers
source	1. .903 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6185002" /sex="male" /tissue_type="dorsal root ganglia" /dev_stage="adult, 36 yr" /lab_host="DH10B" /clone_lib="Lupski_dorsal_root_ganglion" /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN

Query Match 6.5%; Score 236; DB 13; Length 903;
Best Local Similarity 57.4%; Pred. No. 5.2e-44;
Matches 466; Conservative 0; Mismatches 340; Indels 6; Gaps 2;

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Qy       1743 CCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGC 1802
Db         18 CCTGCTGCGAGAGGGGCCTGAGGGCTTTGCTCGAGCTGTGCGGAACCACCCGGGGCTGCT 77

Qy       1803 AGTTACTGATACCACCTTCCGCGATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTC 1862
Db         78 GCTGATGGACACGACCTTCAGGGACGCCCACCAGTCACTGCTGGCCACTCGTGTGCGCAC 137

Qy       1863 ATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGT 1922
Db        138 CCACGATCTCAAAAAGATCGCCCCCTATGTTGCCCACAACTTCAGCAAGCTCTTCAGCAT 197

Qy       1923 GGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTG 1982
Db        198 GGAGAACTGGGGAGGAGCCACGTTTGACGTCGCCATGCGCTTCCTGTATGAGTGCCCCTG 257

Qy       1983 GGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTTCG 2042
Db        258 GCGGCGGCTGCAGGAGCTCCGGGAGCTCATCCCCAACATCCCTTTCCAGATGCTGCTGCG 317

Qy       2043 CGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAA 2102
Db        318 GGGGGCCAATGCTGTGGGCTACACCAACTACCCAGACAACGTGGTCTTCAAGTTCTGTGA 377

Qy       2103 GGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCGCTTAACGACGTCTC 2162
Db        378 AGTGGCCAAAGAGAATGGCATGGATGTCTTCCGTGTGTTTGACTCCCTCAACTACTTGCC 437

Qy       2163 CCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGC 2222
Db        438 CAACATGCTGCTGGGCATGGAGGCGG---CAGGAAGTGCCGGAGGCGTGGTGGAGGCTGC 494

Qy       2223 TATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCTGGATTACTA 2282
Db        495 CATCTCATACACGGGCGACGTGGCCGACCCCAGCCGCACCAAGTACTCACTGCAGTACTA 554

Qy       2283 CCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGATAT 2342
Db        555 CATGGGCTTGGCCGAAGAGCTGGTGCGAGCTGGCACCCACATCCTGTGCATCAAGGACAT 614

Qy       2343 GGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCACTGCG---CCGTGA 2399
Db        615 GGCCGGGCTGCTGAAGCCCACGGCCTGCACCATGCTGGTCAGCTCCCTCCGGGACCGCTT 674

Qy       2400 ATTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTA 2459
Db        675 CCCCGACCTCCCACTGCACATCCACACCCACGACACGTCAGGGGCAGGCGTGGCAGCCAT 734

Qy       2460 CTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCACCACTGTCTGG 2519
Db        735 GCTGGCCTGTGCCCAGGCTGGAGCTGATGTGGTGGATGTGGCAGCTGATTCCATGTCTGG 794

Qy       2520 CACCACCTCCCAGCCATCCCTGTCTGCCATTG 2551
Db        795 GATGACTTCACAGCCCAGCATGGGGGGCCCTG 826
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RESULT 7
AQ875053/c

LOCUS	AQ875053 859 bp DNA linear GSS 08-NOV-1999
DEFINITION	V120F6 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
ACCESSION	AQ875053
VERSION	AQ875053.1 GI:6287297
KEYWORDS	GSS.
SOURCE	Saccharomyces cerevisiae (baker's yeast)
ORGANISM	Saccharomyces cerevisiae Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE	1 (bases 1 to 859)
AUTHORS	Ross-Macdonald,P., Roemer,T., Coelho,P.S.R., Agarwal,S., Kumar,A., desEtages,S.A., Cheung,K.-H., Sheehan,A., Symoniatis,D., Jansen,R., Umansky,L., Heidtman,M., Nelson,K., Iwasaki,H., Kanada,D., Lugo,R., Hager,K., Miller,P., Roeder,G.S. and Snyder,M.
TITLE	Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption
JOURNAL	Unpublished (1999)
COMMENT	Contact: Kumar A Michael Snyder, Dept. of Mol. Cell. and Dev. Biology

Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.

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FEATURES             Location/Qualifiers
     source          1. .859
                     /organism="Saccharomyces cerevisiae"
                     /mol_type="genomic DNA"
                     /strain="Y2278 - S288C background, cir(0) rho(0)"
                     /db_xref="taxon:4932"
                     /lab_host="E. coli"
                     /clone_lib="mTn-3xHA/lacZ Insertion Library, strain Y2278"
                     /note="Vector: pHSS6-Sal; A yeast genomic DNA library
                     without 2 micron or mitochondrial DNA  was prepared in
                     pHSS6-Sal; genomic DNA was size-fractionated  (DNA of
                     roughly 2-3 kb in length) prior to cloning. This library
                     was subsequently mutagenized with a mTn-3xHA/lacZ
                     minitransposon  containing lacZ, URA3, and tet resistance.
                     "
ORIGIN

  Query Match             6.2%;  Score 223.4;  DB 28;  Length 859;
  Best Local Similarity   59.9%;  Pred. No. 4.5e-41;
  Matches  407;  Conservative    0;  Mismatches  268;  Indels    4;  Gaps    2;

Qy        827 AACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAG 886
              ||  | ||  ||  || |   ||||||||||||| ||  |    |||| ||   | |
Db        801 AAAATTCTTGGACAAAGCAAAAGCATATTGAAGTTCATTTGTGGCCCGATAACCACGAAA 742

Qy        887 AAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCG 946
                |||||  || ||||  ||| | |||||  ||  |||||  |    |||||||| ||||||
Db        741 CCGTTGTTCATCTTTTCGAAAGAGACTGTTCGGTGCAGAGAAA-CACCAAAAGGTTGTCA 683

Qy        947 AAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAG 1006
              ||  | ||  |||||| ||  |||      |  ||| |  ||||   ||||||   | |||||||
Db        682 AAGTGGCNCCAGCAAAGACTTTACNCCGTGAAGTCGGTGACGCCATTTTGACAGATGCAG 623

Qy       1007 TAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATG 1066
              | ||  ||   |      |||  |||      |||||  ||  |  ||||||||||  |||
Db        622 TTAAATTGGCCAAAGAGTGTGGCTACAGAAATGCGGGTACTGCTGAATTCTTGGTTGATA 563

Qy       1067 AAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGA 1126
              |  |    | |||   ||||| ||||| || ||| | ||||| || || || ||| | |
Db        562 ACCAAAATAGACACTATTTCATTGAAATTAATCCAAGAATCCAAGTGGAACATACCATCA 503

Qy       1127 CTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAA 1186
              | |||||| | ||||    | ||  | |||  ||| |||||  |   | || || |||||
Db        502 CAGAAGAAATTACCGGTATAGATATTGTGGCGGCTCAGATCCAAATTGCGGCAGGTGCCT 443

Qy       1187 CCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGT 1246
              |  |     | |||| ||   ||| || || || | ||| |  ||    ||  | ||||
Db        442 CTCTACCCCAGCTGGGCCTATTCCAGGACAAAATTACGACTCGTGGCTTTGCCATTCAGT 383

Qy       1247 GCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCG 1306
              |||| || |||||||||| ||    ||  |||||  |||||||||| |  ||    |
Db        382 GCCGTATTACCACGGAAGACCCTGCTAAGAACTTCCAACCAGATACCGGTAGAATAGAAG 323

Qy       1307 CGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTG---CAGCTCAGCTCGGTG 1363
              ||||||  ||  |||| ||   ||| ||| | || || ||||      ||  |    ||
Db        322 TGTACCGTTCTGCAGGTGGTAATGGTGTTAGACTGGATGGTGGTAACGCCTATGCAGGAA 263

Qy       1364 GCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACT 1423
                 ||||  |  | || |  ||||| |||||||| |||    | |||  ||||||  ||
Db        262 CAATAATCTCACCTCATTACGACTCAATGCTGGTCAAATGCTCATGCTCCGGTTCCACCT 203

Qy       1424 TTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTG 1483
                ||||  | | |              || || ||   |||||||   |   |||||
Db        202 ACGAAATCGTTCGTAGAAAAATGATTCGTGCATTAATCGAGTTCAGAATTAGAGGTGTCA 143
```

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Qy       1484 CAACCAACATTGGTTTCTT 1502
              |||||||||   ||| |
Db        142 AGACCAACATTCCCTTCCT 124
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RESULT 8
BF251052

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LOCUS       BF251052                637 bp    mRNA    linear   EST 15-NOV-2001
DEFINITION  EST418309 Coccidioides immitis spherule cDNA library Coccidioides
            immitis cDNA clone CIAAB85 5' sequence, mRNA sequence.
ACCESSION   BF251052
VERSION     BF251052.1  GI:16931195
KEYWORDS    EST.
SOURCE      Coccidioides immitis
  ORGANISM  Coccidioides immitis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Gardner,M.J. and Kirkland,T.
  TITLE     Generation of ESTs from Coccidioides immitis spherule cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES             Location/Qualifiers
     source          1. .637
                     /organism="Coccidioides immitis"
                     /mol_type="mRNA"
                     /db_xref="taxon:5501"
                     /clone="CIAAB85"
                     /dev_stage="spherule"
                     /lab_host="SOLR"
                     /clone_lib="Coccidioides immitis spherule cDNA library"
                     /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
                     Xho1"
ORIGIN

  Query Match             6.1%;  Score 220.2;  DB 10;  Length 637;
  Best Local Similarity   60.4%;  Pred. No. 2.2e-40;
  Matches  380;  Conservative    0;  Mismatches  248;  Indels    1;  Gaps    1;

Qy        685 TACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCT 744
              | ||||||| |  | |||||  |    ||| || || || ||||| |||||| | ||
Db          7 TTCCCCATCATCATCAAGGCCGCCTTCGGCGGCGGTGGCCGCGGCATGCGTGTCGTCCGC 66

Qy        745 TCACCTGATGAGCTTCGCAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTC 804
              |  ||   || ||| | |          ||  |    || ||  || | || |||
Db         67 GACCAGGAGTCCCTCCGCGACTCCTTCGAGCGCGCCACCTCGGAGGCCAAATCCGCCTTC 126

Qy        805 GGCGATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAG 864
              ||| | ||| | || |  |||||  ||      |    ||  |||| || || |||
Db        127 GGCAACGGCACCGTCTTCGTCGAGCGCTTCCTCGACAGGCCCAAGCACATCGAGGTCCAG 186

Qy        865 ATCCTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAG 924
              | || ||||  ||    ||  | || || ||||| || || ||||||||||     | |||
Db        187 CTGCTCGGCGACAACCACGGCAACGTCGTCCACCTCTACGAGCGTGACTGCAGCGTCCAG 246

Qy        925 CGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGT 984
              || || ||||| || || |||||   | || || ||  ||  |  |      ||  | ||.
Db        247 CGCCGCCACCAGAAGGTCGTCGAGCTCGCCCCGGCCAAGGACCTCCCCGTCGACGTCCGC 306

Qy        985 GATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGA 1044
              ||  ||||      || || || || |||  |   |||  |  ||||     ||| ||
Db        307 GACAGCATCCTCGCCGACGCCGTCAAGCTGGCCAAGTCCGTCAGCTACCGCAACGCCGGC 366

Qy       1045 ACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGT 1104
              ||||  || ||| | |||||  |      |  | ||  |||||||| || ||||| ||
Db        367 ACCGCCGAGTTCCTCGTCGACCAGCTCAACCGCTACTACTTCATCGAGATCAACCCCCGC 426
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```
Qy       1105 ATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAG 1164
             ||||||||| |||||||||| | || || ||  |||||| | ||| | ||    || |||
Db        427 ATCCAGGTCGAGCACACCATCACCGAGGAGATCACCGGCATCGACATCGTCGCCGCCCAG 486

Qy       1165 ATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAG 1224
             || |   | || || || || ||| |  || |  | || || ||||| ||    |||
Db        487 ATCCAGATCGCCGCCGGCGCCACCCTCGAGCAGCTCGGCCTCACCCAGGACCGCATCTCC 546

Qy       1225 ACCCACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGAT-CCAAACAACGGCTTCCG 1283
             |||   ||    ||  | ||||||||||||||||| |||||| ||| | |  |||||||
Db        547 ACCAGAGGCTTCGCCATCCAGTGCCGCATCACCACCGAAGATCCCACAAAGGGGCTTCCA 606

Qy       1284 CCCAGATACCGGAACTATCACCGCGTACC 1312
              || || ||||| |  |||   |  ||||
Db        607 GCCCGACACCGGTAAGATCGGAGTCTACC 635


RESULT 9
CA793824
LOCUS       CA793824                862 bp    mRNA    linear   EST 04-DEC-2002
DEFINITION  AGENCOURT_11043532 NICHD_XGC_Emb1 Xenopus laevis cDNA clone
            IMAGE:6865891 5', mRNA sequence.
ACCESSION   CA793824
VERSION     CA793824.1  GI:26042921
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 862)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14488  row: p  column: 18
            High quality sequence stop: 649.
FEATURES             Location/Qualifiers
     source          1. .862
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                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:6865891"
                     /tissue_type="embryo (stage 10)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Emb1"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 1.55 kb. Constructed by Life Technologies. Note: This
                     is a Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             6.0%;  Score 216.6;  DB 14;  Length 862;
  Best Local Similarity   56.7%;  Pred. No. 1.8e-39;
  Matches  421;  Conservative    0;  Mismatches  319;  Indels    3;  Gaps    1;

Qy        841 AACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
              || ||||  || |||||||| ||||| || || ||| |   |||| | || |||||  |
Db         20 AAACCTCGCCACATTGAAGTTCAGATACTCGGTGATAAATATGGAAATGTGGTACATTTG 79

Qy        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960
              |||||| | ||||| ||  | ||| |  | ||||| || || || ||||| || ||||||
Db         80 TATGAAAGAGACTGTTCCGTCCAGAGAAGGCACCAGAAGGTGGTTGAAATAGCCCCAGCT 139

Qy        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
              ||  |||| |   | ||  | ||  |  |         ||  | |||||  |
Db        140 GCACAGCTGGACCTTCAGCTCAGAGACAGACTGACCCATGACTCTGTAAAACTGGCAAAA 199

Qy       1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080
              | |||||  ||  || || || |||||  |||||||  ||| ||  | |||||  ||
Db        200 CAGGTGGGTTATGAGAATGCCGGCACTGTGGAGTTCTTGGTGGATAAACATGGCAAGCAT 259

Qy       1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
              ||||||  ||| | |||  |  | |||| ||||||||  ||  ||  |||||| | ||
Db        260 TACTTCATAGAAGTCAACTCCAGACTCCAAGTTGAGCATACAGTAACGGAAGAAATTACA 319

Qy       1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
              || || ||||| ||  | || |||||  |  | || |  ||  || | |  || |
Db        320 GATGTTGACCTAGTCCATGCCCAGATCCATGTTGCAGAGGGAAAAAGCCTTCCTGACCTT 379

Qy       1201 GGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACG 1260
              || || |  ||||| || |||   | | | |||   ||  | ||||||  |  |||| ||
Db        380 GGCCTCAAGCAAGAGAACATCCGTATCAATGGTTGTGCCATTCAGTGCAGAGTCACAACA 439

Qy       1261 GAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCA 1320
              |||||  ||        || || |  || ||||| ||     ||    |  | |||     |
Db        440 GAAGACCCTTCACGTGGGTTTCAGCCTGATACTGGTCGGATTGAGGTTTTCCGGAGTGGA 499

Qy       1321 GGCGGAGCTGGCGTTCGTCTTGACGGTG---CAGCTCAGCTCGGTGGCGAAATCACCGCA 1377
              |  |||   ||  | || || ||| |||   |||||   |  || |  | ||  || ||
Db        500 GAAGGAATGGGAATCCGACTAGACAGTGCTTCAGCTTTTCAAGGAGCTGTCATTTCCCCA 559

Qy       1378 CACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTT 1437
              || | ||||||| | ||||| ||  | |    |  ||   |||  | ||  ||| | |
Db        560 CATTATGACTCCCTTCTGGTCAAGGTTATTGCACACGGAAAAGACCATCAAGTTGCCGCC 619

Qy       1438 GCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGGT 1497
              |     ||| ||||| ||||||  |   |||||  |  ||| |||
Db        620 ACAAAAATGAGCAGAGCTTTGGCAGAGTTCCGGATTAGGGGTGTTAAAGACAATATTCCC 679

Qy       1498 TTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTC 1557
              |||  |||      |  ||    |  |  | ||          | | |||    ||
Db        680 TTCCTGCAAAACGTCTTGAACAATAATCAGTTTCTCCATGGTACAGTAGACACTCAGTTT 739

Qy       1558 ATTGCCGATCACCCGCACCTCCT 1580
              ||||  ||  | ||  |||||
Db        740 ATTGATGAAAATCCAGACCTCTT 762


RESULT 10
AI109467
LOCUS       AI109467                675 bp    mRNA    linear   EST 19-APR-2001
DEFINITION  GH08678.5prime GH Drosophila melanogaster head pOT2 Drosophila
            melanogaster cDNA clone GH08678 5prime, mRNA sequence.
ACCESSION   AI109467
VERSION     AI109467.1  GI:3477791
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 675)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 86  row: G  column: 6
            High quality sequence stop: 588.
FEATURES             Location/Qualifiers
     source          1. .675
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="GH08678"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."

ORIGIN

Query Match 6.0%; Score 216.4; DB 9; Length 675;
Best Local Similarity 58.9%; Pred. No. 1.8e-39;
Matches 392; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

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Qy       1719 ACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCGTTTGCTCGTGA 1778
Db          8 ACCACCGAAGGGACTCCGCGAGGTCCTGGTGTGCGAAGGTCCGGAGGCCTTCGCCAAGGA 67

Qy       1779 TCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGATGCACACCAGTC 1838
Db         68 GGTGCGCAACCGTAAGGAACTGCTACTCATGGACACCACCTTCCGCGATGCCCACCAGTC 127

Qy       1839 TTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAGGCCGTCGCAAA 1898
Db        128 GCTGCTGGCCACCCGCGTGCGTTCCCACGATCTGCTGAAGATCTCCCCCTACGTGACGCA 187

Qy       1899 GCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTACGATGTGGCGAT 1958
Db        188 CAAGTTCAACAACCTGTATTCGCTGGAGAACTGGGGCGGAGCCACCTTCGACGTGGCGCT 247

Qy       1959 GCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAA 2018
Db        248 GCGCTTCCTGCACGAGTGCCCGTGGGAGCGCCTGGAGGAGATGCGCAAGCGCATCCCGAA 307

Qy       2019 TGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGA 2078
Db        308 CATTCCCTTCCAGATGCTGTTGCGCGGAGCCAACGCCGTCGGCTACACCAGCTATCCGGA 367

Qy       2079 CTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCAT 2138
Db        368 CAACGTGGTCTACAAGTTCTGTGAGCTGGCTGTGCAGACCGGCATGGACATCTTCAGGGT 427

Qy       2139 CTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGAC 2198
Db        428 GTTCGACTCGCTCAACTACCTGCCCAACCTGATCCTCGGCATGGAAGCCGCTGGAAAGGC 487

Qy       2199 CAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGA 2258
Db        488 GGGCGGCGTGGT---GGAGGCTGCCATCTCCTATACCGGAGACGTCAGCGATCCCAAGCG 544

Qy       2259 AAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGC 2318
Db        545 CACCAAGTATGATCTGAAATACTACACTAACCTTGCCGATGAGCTGGTCAAGGCGGGCAC 604

Qy       2319 TCACATCTTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCT 2378
Db        605 CCACGTGCTCTGCATAAAGGATATGGCTGGTCTGCTCAAGCCCGAATCCGCCAGGCTTCT 664

Qy       2379 GGTCAC 2384
Db        665 GATCAC 670
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RESULT 11
BI103175
LOCUS BI103175 744 bp mRNA linear EST 26-JUN-2001
DEFINITION 602889415F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5044779 5', mRNA sequence.
ACCESSION BI103175
VERSION BI103175.1 GI:14554068
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 744)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11122 row: m column: 04
High quality sequence stop: 737.
FEATURES Location/Qualifiers
source 1. .744
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5044779"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. |"

ORIGIN

Query Match 5.9%; Score 214.8; DB 12; Length 744;
Best Local Similarity 58.6%; Pred. No. 4.4e-39;
Matches 430; Conservative 0; Mismatches 297; Indels 7; Gaps 3;

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Qy       1765 GCGTTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGC 1824
Db          15 GGGCTTGCCCGAGCTGTGCGGAATCACCACGGGCTGCTGTTGATGGACACAACCTTCCGG 74

Qy       1825 GATGCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCA 1884
Db          75 GATGCCCACCAGTCACTACTGGCCACTAGAGTGCGCACACATGATCTCAA-AAAGATGCG 133

Qy       1885 GAGGCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACC 1944
Db         134 CCCTATGTTGCCCACAACTTCAACAAGCTCTTCAGCATGGAGAACTGGGGAGGCGCCACG 193

Qy       1945 TACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGC 2004
Db         194 TTCGACGTTGCCATGCGCTTCCTGTACGAGTGCCCCTGGCGGCGGCTCCAGGAGCTCCGG 253

Qy       2005 GAGGCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATAC 2064
Db         254 GAGCTTATCCCGAACATCCCGTTCCAGATGCTACTGAGGGGGGCCAATGCTGTGGGCTAC 313

Qy       2065 ACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTG 2124
Db         314 ACCAACTACCCTGACAACGTGGTCTTCAAGTTCTGTGAGGTGGCCAAAGAGAATGGTATG 373

Qy       2125 GACATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGAC 2184
Db         374 GACGTCTTCCGAGTCTTTGACTCCCTCAACTACTTGCCAAACATGCTGCTGGGCATGGAA 433

Qy       2185 GCAGTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTC 2244
Db         434 GCAG---CAGGCAGTGCTGGGGGTGTGGTGGAGGCTGCCATCTCATACACGGGGGACGTG 490

Qy       2245 TCTGATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATC 2304
```

```
Db        491 GCTGACCCTAGTCGCACTAAATACTCACTGGAGTACTACATGGGCTTAGCTGAAGAACTG 550

Qy       2305 GTCAAGTCTGGCGCTCACATCTTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCT 2364

Db        551 GTGCGAGCTGGCACTCACATCCTGTGCATTAAGGACATGGCGGGCCTGCTGAAGCCTGCC 610

Qy       2365 GCGGTAACCAAGCTGGTCACCGCACTGCG---CCGTGAATTCGATCTGCCAGTGCACGTG 2421

Db        611 GCCTGCACCATGCTGGTCAGCTCCCTCCGGGACCGATTCCCCGACCTCCCACTGCACATC 670

Qy       2422 CACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGT 2481

Db        671 CATACCCATGATACATCAGGGGCAGGTGTGGCAGCCATGCTGGCCTGTGCACAAGCAGGG 730

Qy       2482 GCAGATGCTGTTGA 2495

Db        731 GCTGATGTCGTGGA 744
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RESULT 12
CK000115
LOCUS CK000115 800 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_16368972 NIH_MGC_220 Homo sapiens cDNA clone IMAGE:30707731 5', mRNA sequence.
ACCESSION CK000115
VERSION CK000115.1 GI:38526149
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1072 row: m column: 20
High quality sequence start: 12
High quality sequence stop: 654.
FEATURES Location/Qualifiers
source 1. .800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30707731"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_220"
/note="Organ: mixed; Vector: pYX-Asc; Site_1: EcoRI; Site_2: NotI; Library is oligo-dT primed and directionally cloned Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according tomRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. Average insert size 0.5-1Kb. Adaptors 5'(AATTCGGCACGAGG)3' and 5'd (CCTCGTGCCG)3'. 3' Linker sequence - GCGGCCGCTGAGAGCC T18. Sequencing primers 3'end: T3 promoter primer 5'd (ATTAACCCTCACTAAAGGGA)3'. 5' End: T7 promoter primer 5'd (TAATACGACTCACTATAGGG)3'. Library was constructed in the laboratory of M. Bento Soares. Average insert size 3-4kb Note: this is a NIH_MGC Library."

ORIGIN

Query Match 5.9%; Score 213.2; DB 14; Length 800;
Best Local Similarity 59.1%; Pred. No. 1.1e-38;
Matches 401; Conservative 0; Mismatches 273; Indels 4; Gaps 2;

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Qy        841 AACCCTCAGCATATTGAAGTGCAG-ATCCTTGGCGATCACACTGGAGAAGTTGTACACCT 899

Db         35 AAGCCACGGCACATCGAGGTGCAGAATCTTGGGGGACCAGTATGGGAACATCCTGCACCT 94

Qy        900 TTATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGC 959

Db         95 GTACGAGCGAGACTGCTCCATCCAGCGGCGGCACCAGAAGGTGGTCGAGATTGCCCCCGC 154

Qy        960 ACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCG 1019

Db        155 CGCCCACCTGGACCCGCAGCTTCGGACTCGGCTCACCAGCGACTCTGTGAAACTCGCTAA 214

Qy       1020 CTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCA 1079

Db        215 ACAGGTGGGCTACGAGAACGCAGGCACCGTGGAGTTCCTGGTGGACAGGCACGGCAAGCA 274

Qy       1080 CGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCAC 1139

Db        275 CTACTTCATCGAGGTCAACTCCCGCCTGCAGGTGGAGCACACGGTCACAGAGGAGATCAC 334

Qy       1140 CGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATT 1199

Db        335 CGACGTAGACCTGGTCCATGCTCAGATCCACGTGGCTGAGGGCAGGAGCCTACCCGACCT 394

Qy       1200 GGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCAC 1259

Db        395 GGGCCTGCGGCAGGAGAACATCCGCATCAACGGGTGTGCCATCCAGTGCCGGGTCACCAC 454

Qy       1260 GGAAGATCCAAACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACC 1319

Db        455 CGAGGACCCCGCGCGCAGCTTCCAGCCGGACACCGGCCGCATTGAGGTGTTCCGGAGCGG 514

Qy       1320 AGGCGGAGCTGGCGTTCGTCT---TGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGC 1376

Db        515 AGAGGGCATGGGCATCCGCCTGGATAATGCTTCCGCCTTCCAAGGAGCCGTCATCTCGCC 574

Qy       1377 ACACTTTGACTCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGT 1436

Db        575 CCACTACGACTCCCTGCTGGTCAAAGTCATTGCCCACGGCAAAGACCACCCCACGGCCGC 634

Qy       1437 TGCTCGTGCACAGCGCGCGTTGGCTGAGTTCACCGTGTCTGGTGTTGCAACCAACATTGG 1496

Db        635 CACCAAGATGAGCAGGGCCCTTGCGGAGTTCCGCGTCCGAGGTGTGAAGACCAACATCGC 694

Qy       1497 TTTCTTGCGTGCGTTGCT 1514

Db        695 CTTCCTGCAGAATGTGCT 712
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RESULT 13
BI618593
LOCUS BI618593 640 bp mRNA linear EST 07-SEP-2001
DEFINITION RH49459.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH49459 5 similar to BcDNA:GH06348: FBan0001516 GO:[pyruvate carboxylase (GO:0004736)] located on: 2R 46B14-46C1;: 08/19/2001, mRNA sequence.
ACCESSION BI618593
VERSION BI618593.1 GI:15514118
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 640)
AUTHORS Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E.,

```
            George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G.,
            Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
            Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and
            Rubin,G.M.
  TITLE     BDGP/HHMI RH Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003831: arm:2R [4876906,5137815]
            estimated-cyto:46B13-46E4: 08/19/2001
            Plate: RH.494  row: E  column: 11
            High quality sequence stop: 543.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="RH49459"
                     /sex="male and female"
                     /dev_stage="Adult"
                     /lab_host="DH5-alpha TonA"
                     /clone_lib="RH Drosophila melanogaster normalized Head
                     pFlc-1"
                     /note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
                     BamHI; Library was kindly generated by Piero Carninci at
                     the RIKEN. The library  was normalized and excised using
                     Cre recombinase. Plasmid cDNA library."
ORIGIN

  Query Match             5.8%;  Score 211;  DB 12;  Length 640;
  Best Local Similarity   59.4%;  Pred. No. 3.2e-38;
  Matches  377;  Conservative    0;  Mismatches  255;  Indels    3;  Gaps    1;

Qy        790 GCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAACGTGCTGTGATTAACCCTCAG 849
              ||  | || || || ||| |||| ||| | |   | ||         |       || |
Db          1 GCCAAGGCCGCCTTTGGCAATGGTGCGATGTTCATTGAGAAGTTCATCGAGCGACCGCGT 60

Qy        850 CATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGT 909
              || ||||| || ||  | || || ||   | | ||  | || || || || || ||||||
Db         61 CACATTGAGGTTCAACTGCTGGGAGACAAGGCCGGGAATGTAGTGCATCTGTACGAACGT 120

Qy        910 GACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTG 969
              ||||||||  |||||||||| ||||| || || || || || |||||  |   |    ||
Db        121 GACTGCTCCGTGCAGCGTCGCCACCAGAAGGTGGTGGAGATCGCCCCAGCGCCACGCCTG 180

Qy        970 GATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGT 1029
                  ||| | || ||    ||   | ||  |||||    ||    ||||    | ||
Db        181 CCCATCGAAATCCGGGACAAGATGACGGAGGCAGCAGTGCGCTTGGCCCGCCATGTGGGC 240

Qy       1030 TACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATC 1089
              ||  |    ||| ||||||||||| ||| |   ||| ||    ||||||  |  |||||||
Db        241 TATGAAAACGCCGGAACCGTGGAGTTCCTTTGCGACGAGTCCGGCAACTTCTACTTCATC 300

Qy       1090 GAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGAC 1149
              ||| ||||| | ||| | || || |||||||| || || || || | ||  |   | ||
Db        301 GAAGTGAACGCCCGTCTACAAGTGGAGCACACGGTCACCGAGGAGATAACAGGCATCGAT 360

Qy       1150 CTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACC 1209
               ||||| || |||| || ||| |||| |  ||     ||| |    |||||||||    ||
Db        361 TTGGTGCAGTCGCAAATCCGCGTGGCCGAGGGCATGACCCTACCCGAATTGGGCTACACG 420

Qy       1210 CAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCA 1269
              || || ||||||  | | |  ||   || | ||||||||  | ||||| ||||||||
Db        421 CAGGACAAGATCGTGCCGCGTGGCTATGCCATTCAGTGCCGTGTGACCACCGAAGATCCG 480

Qy       1270 AACAACGGCTTCCGCCCAGATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCT 1329
                |||||  || |  ||  | |||||      |   | ||| ||    |  ||
Db        481 GCCAACGATTTTCAGCCCAACACCGGTCGCTTGGAGGTCTTCCGATCTGGCGAGGGTATG 540

Qy       1330 GGCGTTCGTCTTGACGGTG---CAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGAC 1386
              ||| || |  | ||| |||    | ||  |   ||| | |    ||  |  || ||| |||
Db        541 GGCATTAGGTTGGACAGTGCGTCCGCCTACGCCGGAGCCATCATTTCGCCATACTACGAC 600

Qy       1387 TCCATGCTGGTGAAAATGACCTGCCGTGGTTCCGA 1421
              ||| ||||||| ||  ||| ||  |  |    |||
Db        601 TCCCTGCTGGTCAAGGTGATCTCGCACGCCAGCGA 635


RESULT 14
BG910468
LOCUS       BG910468                715 bp    mRNA    linear   EST 05-JUN-2001
DEFINITION  602806142F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4938203
            5', mRNA sequence.
ACCESSION   BG910468
VERSION     BG910468.1  GI:14290944
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 715)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10873  row: d  column: 12
            High quality sequence stop: 715.
FEATURES             Location/Qualifiers
     source          1. .715
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4938203"
                     /tissue_type="anaplastic oligodendroglioma with 1p/19q
                     loss"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn67"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             5.7%;  Score 208.2;  DB 12;  Length 715;
  Best Local Similarity   56.8%;  Pred. No. 1.5e-37;
  Matches  403;  Conservative    0;  Mismatches  303;  Indels    3;  Gaps    1;

Qy        872 GCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTC 931
              | || ||   |||  |  |  | ||||| || || || ||||||||  | ||||| || |
Db          1 GGGACCAGTATGGGAACATCCTGCACCTGTACGAGCGAGACTGCTCCATCCAGCGGCGGC 60

Qy        932 ACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCA 991
              |||| || || ||||| ||||| || ||     || |||| ||  | || ||    |||
Db         61 ACCAGAAGGTGGTCGAGATTGCCCCCGCCGCCCACCTGGACCCGCAGCTTCGGACTCGGC 120

Qy        992 TTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGG 1051
              |        ||  | ||| ||  ||           | || ||| ||  ||| || |||||||
Db        121 TCACCAGCGACTCTGTGAAACTCGCTAAACAGGTGGGCTACGAGAACGCAGGCACCGTGG 180

Qy       1052 AATTCTTGGTCGATGAAAAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGG 1111
              | ||| |||| ||      | ||||| |||  |||||||||  | ||| | ||  | ||||
Db        181 AGTTCCTGGTGGACAGGCACGGCAAGCACTACTTCATCGAGGTCAACTCCCGCCTGCAGG 240

Qy       1112 TTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCT 1171
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Db        241 TGGAGCACACGGTCACAGAGGAGATCACCGACGTAGACCTGGTCCATGCTCAGATCCACG 300

Qy       1172 TGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACG 1231

Db        301 TGGCTGAGGGCAGGAGCCTACCCGACCTGGGCCTGCGGCAGGAGAACATCCGCATCAACG 360

Qy       1232 GTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCAGATA 1291

Db        361 GGTGTGCCATCCAGTGCCGGGTCACCACCGAGGACCCCGCGCGCAGCTTCCAGCCGGACA 420

Qy       1292 CCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAG 1351

Db        421 CCGGCCGCATTGAGGTGTTCCGGAGCGGAGAGGGCATGGGCATCCGCCTGGATAATGCTT 480

Qy       1352 CTCAGCTC---GGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACCT 1408

Db        481 CCGCCTTCCAAGGAGCCGTCATCTCGCCCCACTACGACTCCCTGCTGGTCAAAGTCATTG 540

Qy       1409 GCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTCA 1468

Db        541 CCCACGGCAAAGACCAACCCACGGCCGCCACCAAGATGAGCAGGGCCCTTGCGGAGTTCC 600

Qy       1469 CCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACT 1528

Db        601 GCGTCCGAGGTGTGAAGACCAACATCGCCTTCCTGCAGAATGTGCTCAACAACCAGCAGT 660

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RESULT 15
BJ063722
LOCUS       BJ063722                641 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ063722 NIBB Mochii normalized Xenopus tailbud library Xenopus
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ACCESSION   BJ063722
VERSION     BJ063722.1  GI:17470882
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
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REFERENCE   1  (bases 1 to 641)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
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                     /clone_lib="NIBB Mochii normalized Xenopus tailbud
                     library"
ORIGIN

  Query Match             5.6%;  Score 204.4;  DB 12;  Length 641;
  Best Local Similarity   58.9%;  Pred. No. 1.1e-36;
  Matches  371;  Conservative    0;  Mismatches  256;  Indels    3;  Gaps    1;

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Db          5 AAACCTCGCCACATTGAAGTTCAGATACTCGGTGATAAATATGGAAATGTGGTACATTTG 64

Qy        901 TATGAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAAGTTGTCGAAATTGCGCCAGCA 960

Db         65 TATGAAAGAGACTGTTCCGTCCAGAGAAGGCACCAGAAGGTGGTTGAAATAGCCCCAGCT 124

Qy        961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020

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Qy       1021 TCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTCTTGGTCGATGAAAAGGGCAACCAC 1080

Db        185 CAGGTGGGTTATGAGAATGCCGGCACTGTGGAGTTCTTGGTGGATAAACATGGCAAGCAT 244

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Db        245 TACTTCATAGAAGTCAACTCCAGACTCCAAGTTGAGCATACAGTAACGGAAGAAATTACA 304

Qy       1141 GAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200

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